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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

0	Result No.
87654321	ult No.
773.6 607 486.6 172.8 172.8 171.2 171.2	Score
89.8 70.5 56.5 20.1 19.9 19.9 18.0	% Query Match
180286 626 854 3951 3957 3957 3078 4409 4421	% Query Match Length DB
80 97 93 97 85 87	DB
AL356574 HSU57655 HSDYPDGEN HSU09178 AR027740 AR023063 HSU20938 BTU20981	ID
AL356574 Homo sapi 057655 Human dihyd X95670 H.Sapiens D 009178 Human dihyd AR027740 Sequence AB003063 Homo sapi U20938 Human 1ymph U20981 Bos taurus	Description

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ACCESSION
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AUTHORS
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Web sit
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On Aug 12, 2000 this sequence version replaced gi:9213933.
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HOMO Sapiens chromosome 1 c.
PROGRESS ***, 26 unordered |
AL356574
AL356574.3 GI:9797568
                                                                                                                                         Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                       Center: Sanger Centre
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AC060784 Homo sapi
AC027625 Homo sapi
AC016700 Homo sapi
AC01529 Homo sapi
AL034556 Plasmodium
166494 Sequence 14
297348 Plasmodium
AC004482 Arabidops
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AC044793 Homo sapi
AC004153 Plasmodiu
AC010228 Homo sapi
X04775 Dictyosteli
AL445207 Human DNA
AC026816 Homo sapi
AC021276 Homo sapi
AC021276 Homo sapi
AC025645 Homo sapi
AP000794 Homo sapi
AP069298 Arabidops
AL161494 Arabidops
AL161723 Homo sapi
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88618 92455 92554: gap of 100 bp 92555 98200: contig of 5466 bp in length 9255 98200: contig of 5279 bp in length 100 bp 11029: contig of 12729 bp in length 11030 117311: contig of 6182 bp in length 117312 117411: gap of 100 bp 117312 117412: gap of 100 bp 117412 121093: contig of 3682 bp in length 121094 121193: gap of 100 bp 121194 137336: contig of 16143 bp in length 137337 137436: gap of 100 bp 100 bp 113737 141486: contig of 4050 bp in length 137437 141486: contig of 100 bp 100
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4 38553: gap of 100 bp
4 45878: contig of 7325 bp
9 45978: gap of 100 bp
9 51984: contig of 6006 bp
15 52084: gap of 100 bp
15 52084: contig of 6120 bp
  /clone="RP11-359C24"
/clone_lib="RPCI-11.
                                                                                                                                           Location/Qualifiers
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85213: contig of 9775 bp in length

85313: gap of 100 bp

88517: contig of 3204 bp in length

88617: gap of 100 bp

92454: contig of 3837 bp in length
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730: gap of 100 bp
75338: contig of 3608 bp in i
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190: gap of 100 bp
23545: contig of 8355 bp in
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92555. .
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/note="assembly_fragment:00693
fragment_chain:5"
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71731. .75338
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52085. .58204
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176801. .180286
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163843. .166322
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149135. .154764
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146804. .149034
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121194 .137336
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15191. .23545
              /note="assembly_fragment:01326"
32087 c 31562 g 56812 t 2
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166423. .176700
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160091. .163742
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137437. .141486
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RESULT 2
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dihydropyrimidine 5 5.1 GI:1518606

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                                                   AATCATTTTAAATATAAACCTGAGGCAGAAGCAGCATATCTTCCTATGAAGTCTATATTT
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0; Mismatches 34;
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17-FEB-1997

Smit, G.P., Bakker, H.D., site leads to exoldihydropyrimidine

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  AGAAAGATAAAAAAAGAAAAGAAAAGCTCAAGAACTCATAAAAAACCCACACAATGTGAAGCT 629
                                                                       CTTATAAATATTAATGTGTATATTTTATCAACGAATCTGCCAGTTGCTTTGCTGATGCAT
                                                                                                                             GCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCATCAGTGAGAAAACGGCTGCATATT 389
                                                                                                                                                                                                                                                                               CCTCTGCAAATATGTGAGGAGGGACCTCAT-AAATATTGTCATATGGAAATGAGCAGATA
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                                                         CTTATAAATTAATGTGTATATTTTATCAAAGAATCTGCCAGTTGCTTTGCTGATGCAT
                                                                                                             GGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCCCAGACAACaTAAGTGTGATAAAAA 449
                                                                                                                                                                                                                                                                                                                                    ATAAAGATTATAGCTTTTCTTTGTCAAAAGGAGACTCAATATCTTTACTCTTTCATGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (07-MAY-1996) Pedro M. Fernandez-Salguero, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lack of dihydropyrimidine dehydrogenase activity and thymine-uraciluria caused by a common splice mutation
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/product="dihydropyrimidine dehydrogenase"
/protein_id="AAB07049.1"
/db_xref="GI:1518607"
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/db_xref="taxon:9606"
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/gene="DPYD"
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Pred. No. 6.8e-109;
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Meinsma et al, DNA Cell Biol. 14:1-6 (1995), U20938, and et al, J. Biol. Chem. 269:23192-23196 (1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vreken, P., Van Kullenburg, A.B., Meinsma, I
De Abreu, R. and van Gennip, A. H.
A point mutation in an invariant splice of
skipping in two unrelated Dutch patients
dehydrogenase deficiency
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Direct Submission
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/protein_id="CAA64973.1"
/db_xref="GI:1246753"
/db_xref="SWISS-PROT:Q12882"
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                                                                                                                                                                                                             translation="DIVTNVSPRIIRGTTSGPMYGPGQSSFLNIELISEKTAAYWCQS/
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                                      Eggink,G., Engel,H., Vriend,G., Terpstra,P. and Witholt,B. Rubredoxin reductase of Pseudomonas oleovorans. Structural relationship to other flavoprotein oxidoreductases based o and two FAD fingerprints

J. Mol. Biol. 212 (1), 135-142 (1990)
                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3951)

Yokota,H., Fernandez-Salguero,P., Furuya,H., Lin,K., McBride,O.W. Podschun,B., Schnackerz,K.D. and Gonzalez,F.J.

CDNA cloning and chromosome mapping of human dihydropyrimidine dehydrogenase, an enzyme associated with 5-fluorouracil toxicity and congenital thymine uraciluria

J. Biol. Chem. 269 (37), 23192-23196 (1994)
3 (sites)
Porter,D.J.,
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Institute, National Institutes of
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Interaction of pyrophosphatase moieties with alfa-helixes dinucleotide binding proteins
Biochemistry 24, 1346-1357 (1985)
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Bethesda, MD 20892, USA
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SIANKNYYGAAKMIFSDNPLGLTCGMVCPTSDLCVGGCNLYATEEGPINIGGLQOFAT
SIANKNYYGAAKMIFSDNPLGLTCGMVCPTSDLCVGGCNLYATEEGPINIGGLQOFAT
SIANKNYYGAAKMIFSDNPLGLTCGMVCPTSDLCVGGCNLYATEEGPINIGGLQOFAT
EVFKAMSIFOL THE SUPPERKSEAYSAKIALFGAGPASISCASETARIGYSDITIFE
KQEYYGGLSTSEIPQFRLPYDVVNFEIELMKDLGVKIICGKSLSVNEMTLSTLKEKGY
KAAFIGIGLPENKDALFQGLTQDQGFYTSKDFLPLVAKGSKAGMCACHSPLPSIROV
VIVLGAGDTAPDCATSALRCGARRVFTYFFRKGFVNIFAVPEEMELAKEEKCEFLPFLS
PRKVIVKGGRIVAMQFVRTEQDETGKMNEDEDQMVHLKADVVISAFGSVLSDFKVKEA
LSPIKFNRGGLPEUDETMQTSEAMVFRAGEDVGLANTTVESVNIDGKQASMYIHKYO
SOYGASYSAKPELPLFYTPIDLVDISVEMAGLKFINFGLASATPATSTSMIRRAFEA
GWGFALTKTFSLDKDIVTNVSFRIIRGTTSGPMYGPGOSSFLNIELISEKTAAYWCQS
VTELKADFPDNIVIASIMCSYNKNDWTELAKKSEDSGADALELMLSCPHROMEERGMGL
ACGODPELVRNICGMVGTAKTTYGGVSGTAIRPLAKRSEDSGADALELMLSCPHROMERGMGL
ACGODPELVRNICGMVGTAKTTYGGVSGTAIRPLAKRSEDSGADAELGMLSCHODWDGOSPAT
ACGOLDFLHSGASVLOVCSAIQNODETTVIEDKTGLALLYLKSIEELQDWDGOSPAT
ACGOLDFLHSGASVLOVCSAIQNODETTVIEDKTGLALLYLKSIEELQDWDGOSPAT
                                                                                                                                                                                                    /citation=[4]
/function="catalytic
785 c 896 g
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/function="electron
2062. .2175
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KRPIPTIKDVIGKALQYLGTFGELSNVEQVVAMIDEEMCINCGKCYMTCNDSGYQAIQ
FDPETHLPTITDTCTGCTLCLSVCPIVDCIKMVSRTTPYEPKRGVPLSVNPVC"
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/protein_id="AAA57474.1"
/db_xref="Gi:58805"
/translation="MAPVLSKDSADIESILALNPRTQTHATLCSTSAKKLDKKHWKRN
                                                                                                                                                                                                                                                              /standard_name="iron-sulfur center"
                                                                                                                                                                                                                                                                                                    /citation=[3]
/function="uracil (substrate)
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/function="catalytic
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/db_xref="taxon:9606"
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f Health, 9000 Rockville
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AR027740
AR027740.
Ogura, K., Nishiyama, T., Takubo, H., Kato, A., Okuda, H., Arakawa, K
Fukushima, M., Nagayama, S., Kawaguchi, Y. and Watabe, T.
Suicidal Inactivation of human dihydropyrimidine dehydrogenase
(E)-5-(2-bromovinyl)uracil derived from the antiviral, sorivudi
                                                                                             AB003063.1 GI:6729337 dihydropyrimidine dehydrogenase. Homo sapiens male lymphocyte cDNA to mRNA.
                                                                                    Homo
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Gonzalez, F.J. and Fernandez-Salguero, P.
                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                          Homo sapiens
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Pred. No. 2.8e-24;
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                                 Okuda, H., Arakawa, K.,
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                       Human lymphocyte dihydropyrimidine dehydrogenase mRNA,
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            cds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cancer Lett. 122 (1-2), 107-113 (1998) 98124145
Erratum:[[published erratum appears in 19:128(2):229]]...
                                           HSU20938
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79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (E-mail:ogurak@ps.toyaku.ac.jp, Tel:+81-426-76-4518
Fax:+81-426-76-4517)
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/protein_id="BAA89789.1"
/db_xref="GI:6729338"
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/db_xref="taxon:9606"
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244 CTCAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCCATAATCATCCG 303
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                                                                                                    Local Similarity 93.1
les 179; Conservative
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Submitted (10-FEB-1995) Pharmacology, University of Alabama at Birmingham, 1670 University Blvd., Birmingham, AL 35294-0019, USA 1907 this sequence version replaced gi:693911.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Johnson, M.R., Albin, N., Shahinian, H. and Diasio, R.B. Identification of a frameshift in the DNA coding for dibydropyrimidine dehydrogenase (DPD) in a DPD deficient patient exhibiting 5-fluorouracil toxicity
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1 (bases 1 to 4409)

Diassio,R.B., Beavers,T.L. and Carpenter,J.T.

Familial deficiency of dihydropyrimidine dehydrogenase. Biochemical basis for familial pyrimidinemia and severe 5-fluorouracil-induced
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Lu,Z.H., Zhang,R. and Diasio,R.B.
Purification and characterization of dihydropyrimidine
dehydrogenase from human liver
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FRKVIVKGGRIVAMQFVRTEQDETGKNUEDEDQMVHLKADVVISAVGSVLSDFKVKEA
LSPIKFNRWGLPEVDPETMQTSEAWVFRAGDDDQMVHLKADVVISSVNDGKQASWYIHKYVQ
SQYGASVSAKPELPLFYTPIDLUDISVEMAGLKFINPEGLASATPATSTSMIRRAFEA
GWGFALTKTFSLDKDIVTNVSPRIIRGTTSGPMYGPGQSSFLNIELISEKTAAYWCQS
VTELKADFPDNIVIASIMCSYNKNDWTELAKKSEDGADALELNLSCPHGMGERGMGL
ACGQDPELVRNICRWVRQAVQIPFFAKLTPNVTDIVSIARAAKEGGANGVTATNTVSG
LMGLKSDGTPWPAUGIAKRTTYYGGVSGTAIRPIARAUTSIARALPGFPILATGGIDS
AESGLKFDLSKNLOWTELAKKSTDYGGVSGTAIRPIARAUTSIARALPGFPILATGGIDS
AESGLKFDHSGASVLQVCSAIQNQFTVIEDYCTGLKALLYLKSIEELQDWDGQSPAT
VSHQKGKPVPRIAELMOKKLPSFGPYLLORKKIIAENKIRLKEQUNAFSPLKRNCFIP
                                                                                                                                                                                                                                                     KRPIPTIKDVIGKALQYLGTFGELSNVEQVVAMIDEEMCINCGKCYMTCNDSGYQAIQ
FDPETHLPTITDTCTGCTLCLSVCPIVDCIKMVSRTTPYEPKRGVPLSVNPVC"
1 845 c 949 g 1298 t
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SIANKNY YGAAKMIFSONPLGLTCGMVCPTSDLCVGGCNLYATEGGP INIGGLQOFAT
EVFKAMS IPQIRNPSLPPPEKMSEAY SAKIALFGAGPASISCASFLARLGYSDITIE
EVFKAMSIPQIRNPSLPPPEKMSEAY SAKIALFGAGPASISCASFLARLGYSDITLEE
KQEYVGGLSTSBIPQFRLPYDVVNFELELMKDLGVKIICGKSLSVNEWTLSTLKEKGY
KAAFTGIGLPEPNKDAIFQGLTQDQGFYTSKDFLPLVAKGSKAGMCACHSPLPSIRGV
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/protein_id="AAB51366.1"
/db_xref="G1:693912"
/transiation="MAPVLSKDSADIESILALNPRTQTHATLCSTSAKKLDKKHWKRN
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/EC_number="1.2.1.2"
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102. .3179
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/db_xref="taxon:9606"
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U20981.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Albin, N., Johnson, M.R. and Diasio, R.B. cDNA cloning of bovine liver dihydropy DNA Seq. 6 (4), 243-250 (1996)
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Cancer Res. 53 (22), 5433-5438 (1993)
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Johnson, M.R.
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                  KÄAFIGIGLPEPKKÜHIFQGLTQDQGFYTSKDFLPLVAKSSKAGMCACHSPLLSIRGT
VIVLGAGDTAFDCATSALRCGARRVFIVFRKGFVNIRAVPEEVELAREEKCEFLPFLS
PRKVIVKGGRITATVAMQFVETTGQDETGKNNEDGDQIACLKADVVISAFGSVLSDFKVKE
LSPIKENRWDLPEVDPETMQTSEPWVFAGGDVVGIANTTVEAVNDGKQASWYIHRYIQ
SQYGASVSAKPELPLFYTPIDLVDISVEMAALKFTNPFGLASAFTTTSSSMIRRAFEA
GWAFALTKTFSLDKDIVTNVSPRITGTTSGPMYGPGQSSFLNIELISEKTAAYWCQS
VTELKADFPDNIVIASIMCSYNNNDWMELISRKAEASGADALELNLSCHFMGMEERGMGL
ACGQDPELVRNICRWYRQAVRIPFFAKLTPNVTDIVSIARAAKEGGANGVTATNTVSG
                                                                                                                                                                                                                                                                     /product="dihydropyrimidine dehydrogenase"
/protein_id="AAB40985.1"
/db_xref="G1:677951"
/tzanslation="MAPVLSKDVADIESTLALNPRTQSRATLRSTLAKKLDKKHWKRN
PDKNCFNCEKLENNFDDIKHTTLGERGALREAMRCLKCADAPCQKSCPTNLDIKSFIT
                                                                                                                                                                                                    EVFKAMNIPQIRNPSLPPPEKMPEAYSAKIALLGAGPASISCASFLARLGYNDITIFE
KQEYVGGISTSEIPQFRLPYDVVNFEIELMKDLGVKIICGKSLSVNDITLSTLKEEGY
LMGLKADGTPWPAVGREKRTTYGGVSGTAIRPIALRAVTTIARALPEFPILATGGIDS
                                                                                                                                                                                                                                                   SISNKNYYGAAKMIFSDNPLGLTCGMVCPTSDLCVGGCNLYATEEGPINIGGLQQYAT
                                                                                                                                                                                                                                                                                                                                                                                                      /note="dihydrothymine dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="liver"
75. .3152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Bos taurus"
/db_xref="taxon:9913"
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                                          dinucleotide binding proteins
Biochemistry 24, 1346-1357 (19
                                                                                                                           Dupuis, A., Skehel, J.M. and Walker, J.E.

A homologue of a nuclear-coded iron-sulfur protein subunit of bovine mitochondrial complex I is encoded in chloroplast genomes Biochemistry 30 (11), 2954-2960 (1991)
                                                                                                                                                                                                                                                                                             relationship to other flavoprotein oxidoreductases based on and two FAD fingerprints
J. Mol. Biol. 212 (1), 135-142 (1990)
                                                                                                                                                                                                                                                                                                                                                                                            Yokota, H., Fernandez-Salguero, P., Furuya, H., Lin, K., McBride, O.W. Podsschun, B., Schnackerz, K.D. and Gonzalez, F.J. cDNA cloning and chromosome mapping of human dihydropyrimidine dehydrogenase, an enzyme associated with 5-fluorouracil toxicity and congenital thymine uraciluria and congenital thymine uraciluria J. Eiol. Chem. 269 (37), 23192-23196 (1994)
              Gonzalez, F
                                                                    Wierenga, R.K., De Maeyer, M.C.H. and Holl
Interaction of pyrophosphatase moieties
                                                                                                                                                                                                                          Porter,D.J., Chestnut,W.G., Merrill,B.M. and Spector,T. Mechanism-based inactivation of dihydropyrimidine dehyd 5-ethynyluracil
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Sus scrofa dihydropyrimidine
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Mammalia;
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FDPETHLPTVTDTCTGCTLCLSVCPIIDCIKMVSRTTPYEPKRGLPLAVNPVS"
a 874 c 958 g 1274 t
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EVEKAMNIFQIRNECLESQEKNEBAYSAKIALLGAGPASISCASFLARLGYSDITLEE
KQEYVGGLSTSEIPQFELLPUVVNFEIELMKDLGVKIICGKSLSENEITLNTLKEBGY
KAAFIGIGLPEPKTDDIFQGLTQDQGFYTSKDELPLVAKSSKAGMCACHSPLPSIRGA
VIVLGAGDTAFDCATSALRCGARRVFLVFRKGFVNIRAVPEEVELAKEEKCEFLPFIRA
VIVLGAGDTAFDCATSALRCGARRVFLVFRKGFVNIRAVPEEVELAKEEKCEFLPFIS
PRKVIVKGGRIVAVQFVRTEQDETGKWARDDDQIVHLKADVVISAFGSVLRODKVKEA
LSPIKFURRDLPEVDEPEMYGSEPWYFAGGIVGMANTTYESVNDGKQASWYIHKYIQ
AQYGASVSAKPELLPLFYTFVDLVISVEMAGLKFINFGLASSAPTTSSSMIRRAFFA
GWGFALTKTFSLDKDIVNNVSPRIVRGTTSGFWYGPGQSSFLNIELLSEKTPAXWCQS
VTELKADFPDNIVIASIMCSYNKNDWMELSRKAEASGADALELNLSCPHGMGERGMGL
ACGQDELIVRNICRWYQAVQIFFFAKLTPNVTDIVSIARAAKEGGADGVTATNTVSG
LMGLKADGTFWFAVGAGKRTTYGGVSGTAIRFIALRAVTTIARALPGFPILATGGIDS
AESGLQFLHSGASVLQVCSAVQNODFTVLQDYCTGGKALLYLKSIEELQGWOGQSPGT
ESHOKGKVPFRIAELMGKKLFMCFPYLEDKKTIAERKMRLKEQNAAFPPLERKPFIP
KKPIPAIKDVIGKALQYLGTFGELSNIEQVVAVIDEEMCINCGKCYMTCNDSGYQAIQ
FDBFTHLFTVTDTCTGCTLCLSVCPIIDCIRMVSRTTPYEPKRGLPLAVNPVC"
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/function="uracil (substrate) binding
2938. .2973
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928 c 998 g
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/protein_id="AAA57475.1"
/db_xref="g1:558307"
/translation="MAPVLSKDVADIESILALNPRTQSHAALHSTLAKKLDKKHWKRN
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2062. .2175
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/db_xref="taxon:9823"
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                                                                                                                                                                                                                                                                                                                                                     Submitted (01-MAY-1996) to the DDBJ/EMBL/GenBank databases. Masahiro Kimura, Kobe Gakuin University, Faculty of Nutrition; Arise, Irkawadani-Kobe, Nishi-ku, Kobe, Hyogo 651-21, Japan (Tel:078-974-1551(ex.3242), Fax:078-974-5689)

2 (bases 1 to 4358)
Kimura, M., Sakata, S.F., Matoba, Y., Matsuda, K., Kontani, Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D85035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Citone Annuellos
Rattus norvegicus
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kimura, M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unclassified.

1 (bases 1 to 4447)

1 (conzalez, F. J. and Fernandez-Salguero, P. Gonzalez, F. G
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AR027741.1
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us norvegicus (strain:Wistar) 7-d-old
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_____ rannoda ZAPII cDNA"
/dev_stage="7-d-old"
                                               /strain="Wistar"
/db_xref="taxon:10116"
/clone_lib="Lambda ZAP
                                                                                                                                                                                         Location/Qualifiers
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930 c 1000 g
                                                                                                                                 /organism="Rattus norvegicus"
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Pred. No. 3.8e
0; Mismatches
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RESULT 12
CELC25F6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        163;
Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimo, O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A.
                                                                                                                                                                                                                                    Caenorhabditis elegans strain=Bristol N2
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                  Caenorhabditis elegans U39742
                                                                                                                                                                                                                                                                                                            U39742.1 GI:1049455
                                                                                                                                                                                                                                                                                                                                                                                 CELC25F6
                                                                                                                                         1 (bases 1 to 43803)
Wilson, R., Ainscough, R.,
                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis
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KQEYVGGLSTSEIPQRELPYDVVNFEIELMKDLGVKIICKSISTDEMTLSTLKERGY
KAAFIGIGLPEPKKDHIFQGLTQVQGFTYSKDELPLVAKGSKPGMCACHSPLFSVRGA
VIVLGAGDTAFDCATSALRCGARRVFIVERKGFANIRAVFEEMELAKEEKCEFLFFLS
PRKVIVKDGKIVGMQFVRTEQDETGNAVEDEEQIVRLKADVVISPFGSVLDDFKVIEA
LSPIKFNRWGLPEVNPETMQTSEPWVFAGGDVCMANNTIVESVUDGKQASWYIHEYIQ
AQYGALVPSQFTLPLFYTPVDLVDISVEMAGLDVRNAVTIVESVUDGKQASWYIHEYIQ
AQYGALVPSQFTLPLFYTPVDLVDISVEMAGLERFNPFGLASATPATSTFMIRRAFEA
GWGFALTKTFSLDKDIVTNVSPRIIRGTTSGPLYGPGQSSFLNIELISEKTAAYWCHS
VTELKADFPDNILIASALMCSYNKUMMELSKMAEASGADALELNLSCPHCWGERGWGL
ACGQDPELVRNICKWYRGSVKWPFFAKLTPNVTDIVSIARAAKEGGADGVTATNTWVSG
LMGLKADGSPWPSVGSGKRTTYGGVSGTTIRPIALRAVTAIARALPGFPILATGGIDS
AESGLQFLHSGASVLQVCSAIQWODFWVIEDVCTCKALLYLKSIEELSDWDGQSSPT
AESGLQFLHSGASVLQVCSAIQWODFWVIEDVCTCKALLYLKSIEELSDWDGQSSPT
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/protein_id="BAA33218.1"
/protein_id="BAA33218.1"
/db_xref="GI:3628593"
/translation="MACVLSROAPDIESILALNPRIQAHATLRSTMAKKLDKKHWKRN
/translation="MACVLSROAPDIESILALNPRIQAHATLRSTMAKKLDKKHWKRN
TDKNCFICEKLENNFDDIKHTTLGERGALREAVRCLKCADAPCQKSCPTSLDIKSFIT
SIANKNYYGAAKLIFSDNPLGLTCGMYCPTSDLCYGGCNLHATEEGPINIGGLQQFAT
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/EC_number="1
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59. .3136
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St. Louis, MO 63110, USA, and
Sanger Centre, Hinxton Hall
Cambridge CBLO IRQ, England
e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk
MEIGHBORING COSMID INFORMATION:
The 5' cosmid is CA1A3, 1000 bp overlap; 3' end lies in a gap
followed by the cosmid T23F2. Actual start of this cosmid is at
base position 1 of CELC25F6; actual end is at base position 43803
of CELC25F6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTES:
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94150718
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Staden,R., Sulston,J., Thlerry-Mieg,J., Thomas,K.,
Vaughan,K., Waterston,R., Watson,A., Weinstock,L.,
Wilkinson-Sproat,J. and Wohldman,P.
2.2 Mb of contiguous nucleotide sequence from chron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-OCT-1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 (bases 1 to 43803) Waterston, R. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of C. elegans Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bentley, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 Mb of contiguous nucleotide sequence from chromosome III of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 43803)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ing sequences below are predicted from computer program Genefinder(P. Green and L. Hillier, ms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     368 (6466), 32-38 (1994)
                                                                                                                                                                                                                                                                                                     /gene="C25F6.4"

join(16243. .16401,16449. .16601,17110. .17257,17309. .1
17576. .17675,177720. .17825,18125. .18202,18252. .18358,
18406. .18572,18930. .19243,19293. .19592,20318. .20513,
20569. .20718,20773. .20895)
/gene="C25F6.4"
/note="similar to protein tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /evidence=not_experimental
/protein_id="AAA80431.1"
/db_xref="GI:1049456"
/translation="MMISRFLSKILIVSCLIGVLGVADASSSMYARRRTASERLMSII
RPRMFQNPEFRSSQKIQKSIQLNPNRALPCCKDESGGSICKNLRRTDIKLFTQKCQTE
PDFSLVVCCSSCSDAGISYRKAQKOVFIFTILVI"
                                                                                                                   /codon_start=1
/evidence=not_experimental
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/db_xref="GI:1049457"
/db_xref="GI:1049457"
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/translation="MONGDIADSQITASSSFDKQSVGPQNARLHSELASGAWCPKPQI
NSKSVEFLQVTLNDTFLITSVETQGRYGNGTGREFASHYMIDYLRPGSQWIRYKNRTG
NSKSVEFLQVTLNDTFLITSVETQGRYGNGTGREFASHYMIDYLRPGSQWIRYKNRTG
NYKSVEFLQVTLNDTFLITSVETQGRYGNGTGREFASHYMIDYLRPGSQWIRYKNRTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(5095. .5215,5259. .5385,5443. 5584. .5656))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(5095. .5656)
/gene="C25F6.6"
PSSAATQQLLVVCGIIFLTIFACVAYCVSVCLKRRQKNKSVDSNVKKDLIITHMGNKP
TCHVFPSNGKLSNGHYEVANDILYARSQKSTLLSVSSKSTFSCRAIPPTWTDFNFPPP
                                                                        VPDGSRLDTLDFKDSMFEDSQIYTESGIKRYGSWPANRRFRSAASPFEKNQMNNSWIG
WNRDTTDGRITILFEFEEVHNETDVVLATFGNRIDGIDVIFSQDGKTFPLFSQISSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="Lys;
16243. .208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (6056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1397.
                                                     RQSLNNTSRRYDFRVPLHNRAGRKVRISIKFSSDWMFLTEVHFTSAANLTLLSEKIPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="C25F6.6"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="C25F6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Caenorhabditis elegans"
/db_xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="Leu;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted by:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon recognized: AAA"
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6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert Waterston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .6128)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   analysis, using in preparation)
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KHTTLSERGALKEAMRCLKCADA ÞCQKSC ÞTQLDVKSF ITS ISKNIV YGAARQILSDN
PLOLITCIM LOFTSDLCVGSCILQA ÞCQKSC ÞTQLDVKSF ITS ISKNIV YGAARQILSDN
PLOLITCIM LOFTSDLCVGSCILQA ÞCQK SCE ANLIGGLQOY ACDWFKOMMVRO IVSK EVRE
NRNASH KEQVALIGCGPAS I SCASFLARLG TIÐI TI YEKRAY IGGLSSA EI POFRLÞY
DVNDF I GLARDIGVQI ETINR ÞLOKDGLÍLAKLK EQGAAVF I GIGHPEÐK I DPLFEG
LTT I ENGTYTSKNYL ÞA VAAA SKÞOMGGK KTÐ LÞTMRGRVVVLGAGDT AMDCATSALR
CGASRVTI LAFRKGTTG I RAVÞEÐBEJAK KEKCEFTL ÞFS SARK INVKDGRI VS LÐRNKT
EQDDINGKWY EÐBEÐGIVLI KCDY VI SAFGSTLKEÐA VLSALQÞOQLINKRGGI FVDSTTO
QTSEKWVFAGGDVAGVAETTVESVNDGKI AAWNMHRY I OSLHGNOV SET ÞELÞOFFT Þ
IDEVDI SVDMCGVKFENÐFGLASA ÞTTSGÐMCRRAÐFÐGMGF I LTKTYGLDKDLVTN
VSPRI VRGSTSGÐF VYGÐNOGSFMNI EL I SEKSCEYWLQC I RELKRÐHPTK I VI AS IMC
VY NKADWI ELATK SLEAGADI LELNLSCÐHGMGKKMGLACGGSÐEI VKÐI CRWYRAC
VKRAÐWI ELATK SLEAGADI LELNLSCÐHGMGKKMDGNAWARALGSTKR
VGRAVERÐA VÁRÐA VÁ
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| gene="C25F6.2" | 35812,35889. .36107,36155. .36 | 1011,34301. .34613,35496. .35812,35889. .36107,36155. .36 | 36299. .36389,36443. .36794,36851. .37157,37216. .37684,37743. .3856,38850. .38632,38680. .38801,38857. .38870,38931. .38249,39228. .39253,39483. .39725)
                                                                                                  EGGAALADGRMRKNDI ITAVNNTNCENVKHEVAVNALKSSGNVVSLSLKRRKDEAFLP
IGGNFGGSTSYLRSGVYPSVSAGNLQHAIHSPGAPI I PPPPPPWHGSLSQLSVGQYR
STRPNTSVIDLVKGARGLGFSTAGGQNEHVKODTDI Y VFK IIEEGAAELDGRLRVGD
KILEVDHHSLINTTHENAVNVLKNTGNRVRLLIQGTGAIFNDSASQQFMPTTPILRP
SSVQDYNRSQWGSQSHLSYGGPLNTSYSSQAPIAIPLEPRPVQLYKGQNGLGFNIVGG
EDNEPIYISFVLPGGVADLSGNVKTGDVLLEVNGVLKNTHKEAAEALRNAGNPYYL
TLQYRPQEYQITESKIEKLRNDYIAQSRMGTLSRKSEYVRALEDYDDSRENSVAPHS
MGFNYGDILHIINSSDDEWMTARKVHENGEFTAEGVIPSKKRVEKREBLRRKQVNFNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SSVERLLEALKPVVYFYFQSQKLVDQFNFFNFQRPASKENRSEWEERLTEEGSMSHES
SEKAHKAIENVEDYCQTLTRHCNEELKRULERVITTFKSNLMHSLDIHDLYBQTLLS
SEKAHKAIENVEDYRVLERLEGGPHSVNSRPAARTSTSNYLNLSSTTPLISDLRDRGFS
YLNGGGLGNGLGNGLLSSPYNSSSTHYLHERQRQTSHDGTWRETTTRTVDTPSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-"coded for by C. elegans cDNA yk25e5.3; coded for k C. elegans cDNA yk25e5.5; similar to repeat guanylate kinase domain of D. melanogaster lethal(1) discs large-1 tumor suppressor protein (SP:DLG1_DROME, P31007) and R. norvegicus postsynaptic density protein 95 (PSD-95) (SP:PSD9_RAT, P31016)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="C25F6.3"
/note="coded for by C. elegans cDNA yk28e9.3; coded for legans cDNA yk28e9.5; coded for by C. elegans cDNA yk28h9.3; coded for by C. elegans cDNA yk28h9.5; coded for by C. elegans cDNA yk40e4.5; coded for by C. elegans cDNA yk5h3.5; weakly similar to dihydroorotate dehydrogenase and glutamate synthase"
GSQSLGRNSSTTGLENRRGSRSQLSFSRKFPFVKSTDRLNDLNEESSNVAEEPVWSYQ
AVEQQAINYVRPVIILGALKDRINDELVNRDPSKFSSCVPHTSRPPREGEVNGRDYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAA80434.1"
/db_xref="GI:1049459"
/translation="MAACLCVCVCVCVCACVCRKFLFLSDKLCLIAAOFFLFVFNASFLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FGKYRDEREKLEAIKLSESNLLDTENYHFASRPDTQVSRVPTVEDVIGKALPRIGPYV
TLDNQEQKVAIIDDDMCINCGKCYMTCNDSGYQAITFDPVTHQPHVTEDDCTGCTLCY
SVCPIPECIEMVPRTGPWKAPKRGVKPSVEPGTPKVVKVDQRGRVILDTTGGMQ"
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AVQNQDFTVVDDYCTGLKALLYLSGAESLKNWDGQSPPIEKHQKGKPILLQGQKKMPF
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/db_xref="GI:1049458"
/translation="MSDEYARCLSIETECKFENITETAMTPKPUTTSPTNNLPLLSK
DSPDIESLLILNPKVODKANAVPSAVTKKNKHNWKRUEEKGCGSTCGESKLKNDFRDI
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VCSPRGPSHHAQLRYSAPESIVNNEFTHKSDAWAVATTVYEMAYQCRQRPYEELTNEQ
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IFGGLKCAHKSTKEEDCVHGTRALGDEIACLLQCGRHPRIVELFGVDESYNLLLEHVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
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join(22629. .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCCCAGACAACAT 435
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                                                                                                                Submitted (16.NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10214237 by the submitte For further information on this sequence e-mail to fly@celer*
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced.
* by the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 24429)
                                                                                                                                                                                                                                                                                                        Direct Submission
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                 /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
5227 c 5359 g 7008 t
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/tabslation="MAKKMTQEELVQAFNQYMPKRPVYPPLVHDDDVLAHSATESEG
/translation="MAKKMTQEELVQAFNQYMPKRPVYPPLVHDDDVLAHSATESEG
SDEEEDDLTKRLKVTLAFSTDMMSECRTAWEDSTCKPPIQYLEDNIQKDVEYILEKLV
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//gene="C25F6.1"
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TQEISNTPIWVPQTLLLELRNLSFLLPSPSSPNSIHFLLEIVTVCDILNASFVSTNRK
                                                                                                     Location/Qualifiers
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join(41327 .414
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Pred. No. 0.00012;
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108; Conserv
                                                 Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C., Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turn, Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A., Weissenbach,J., Williams,S.M., Woodage,T., Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhu,S., Zhu,X., Smith,H.O., Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C. The genome sequence of Drosophila melanogaster Science 287 (5461), 2185-2195 (2000)
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1 (bases 1 to 30302)
1 (clniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Adams, M.D., Celniker, S.E., Holt, R.W., Hoskins, R.A., Galle, R.F., Amanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., Amanatides, P.G., Scherer, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Brandon, R.C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J., Andrews-Pfannkoch, C., Baldwin, D., Ballew, R.M., Basu, A., Basu, A., Bayendale, J. Bayendale, B., Baster, R.M., Basu, A., Baster, R.M., Basu, A., Baster, R.M., Ba
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63.9%;
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Pred. No. 0.00016;
0; Mismatches 61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ., Turner, R.,
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On Oct 9, 2000 this sequence version replaced gi:7290992.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 303092)
Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter Direct Submission
Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
                                                                                                                                                AKGFLGRIKRYSYLGNKLGRRNLGSMNLNPPNNYDNSYSPTKLHTGSYNNTGSHSDD
HRLBIGAPILISTTILDTDREDVTEARLKOIGGGIAOTSSI VRFITFRSSDEEEPVDA
RSSPOGMERDEDLQIADDQVEKNDRDQYGHOOLGGGIAOTSSI VRFITFRSSDEEEPVDA
RSSPOGMERDEDLQIADDQVEKNDRDQYGHOOLGGGIAOTSSI VRFITFRSSDEEEPVDA
RSSPOGMERDEDLQIADDQVEKNDRDQYGHOOLGGGIAOTSSI VRFITFRSELKY
VYLHKSNSVALDMNYTAPAKLGLDLNLPELPELYGASELSLAASDNKENLPAVKPSAE
RSPIPNGGFMAQOPHFKSLDSFHLNTRSHSNOSSOQSSROLACSSSNGEYDFDLKSV
SYQSLNAQNLFVSIDELQELIFROINETEDFGKEIDLEYCAHRDQLRPSERRITILLKNK
NQTLLNGHNHNKEKLRKGWHGKHWLGEEGSKIKEAVRQOTPLKKLAGSRSNLNGSTAD
ASRQSMSPERTORDYTESCEDVTERTEMESSMSHRNSEEDLSPHAKRFKDEGQNGFEE
LRRYVKQGGDFSKELLFVLQERADSELLYSKSLSKLANKINKAGREIPGSVADAWRGV
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DNKRKKAEEAVKRADVEYYTLCVRSERARVDWEMAVLLGSSEQQRGRIGNHHNFA
COVABLITENTEGETGAT
                             QQYARLISDMNPILGGLSTRLQPQLDACNVAKDMQVVRHIRRNSEGPSEQLLPDFYCE
HTTLAMNRERRKHALIKLLQLVKTDLERERRSRDGLRGLSQSLNHQEHQNITDKLYHI
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note="CG4040 gene product"
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KILRQSVSEDQPIYANVDEVIPIHLEPETGTEVDALMGNAQVSGPKNPGTQLQTTSSI
CIRLHCIPSNKIPN"
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join(6691. .6699,8631. .8972)
/gene="CG15364"
/note="CG15364 gene product"
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20838. .2094
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/db_xref="taxon:7227"
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20948,21010. .21879)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .>8972)
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/ERECTER CONTROL OF THE CONTROL OF THE
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.40549,41242. .41250))

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complement(<38162. .>38842)
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                                                                                                                                                      TLDTLIEESTTYAEDIAKLRQKLDDFRLNLELEKRQWSAEKDKVLGYQKQLQAHYIQM
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complement(j0in(23607...24527,24584.
25214...25346.25568...25910,26018...2
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RGQADGGSNQQDSDFDEFSSQDEDDEPQQPQQQPQPLQSQQQQQQPLLQNPTINGQVQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="CG15365 gene product"
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complement(join(40144. .40361,40432. .40549,41242.

.41250))

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Matches 108; Conserv
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 2348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster Dreg-3 protein mRNA, complete cds. U65491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (29-JUL-1996) Ophthalmology and Visual Washington University School of Medicine, 660 S. 8096, St. Louis, MO 63110, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Curr. Biol. 5 (12), 1424-1436 (1995)
96362140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Gelder, R.N.,
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                                                                                                           /translation="MEECRIEQNENDEWVEDEEQTQRLKANFVISAFGSGLEDQDVKA
ALAPLOPRGELPVDRYTMQSSVKQVELGGDLAGVANTTVESVNDGKVAAWSTHCQLQ
GLPLDTPAALPLFYTDIDAVDISVEMCGIFEDNFGLASAPPTTSTAMIRRAFEQGWG
FVVTKTFGLDKDLVTNVSPRIVRGTTSGY KYGPQQGCFLNIELISERABETWLKSIGE
EVTKTFGLDKDLVTNVSPRIVRGTTSGY KYGPQQGCFLNIELISERABETWLKSIGE
LKRDFPEKIVIASIMCSFNEEDWTELAIKAEQSGADALELNLSCPHGMGERGMGLACG
DPELVGDISRWYRKAVKLPFFIKLTFUNITDIVSTAMAAKREEBMRSAINTVQGLMGL
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LQPIHAGATVLQICSSVQNQDFTVIEDYCTALKALLYLKRIRHQSMVPSGMASHHPRR
SIRRQARCFDDRRGKATLGFFGPYQRQDIKMAELRSQKGALSWDABQVKATPPASNG
SIRRQARCFDDRRGKATLGFFGPYQRQDIKMAELRSQKGALSWDABQVKATPPASNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                        rhythmically expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="similar to dihydropyrimidine dehydrogenase;
rhythmically expressed gene 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Drosophila melanogaster"
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                                                                                                                                               AGGACATTGTGACAAATGTTTCCCCCCATAATCATCCGGGGAACCACCTCTGGGCCCCATGT 326
ACTGGCTGAAATCGATTGGAGAACTGAAGCGTGACTTCCCCGAGAAGAT 1037
                              ATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCCCCAGACAACaT 435
                                                                 ATGGACCGCAGCAGGGTTGTTTCCTGAACATCGAACTAATCTCGGAGAAGCGGGCCGAGT 988
                                                                                ATGGCCCTGGACAAGCTCCTTTCTGAATATTGAGCTCATCAGTGAGAAAACGGCTGCAT 386
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Vector pMVX-BG DNA

Human T gene DNA.

Human secreted pro Borrelia burgdorfe Borrelia burgdorfe Borrelia burgdorfe Human DNA marker c Human UGT2B7 exon

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Borrelia burgdorfe Arabidopsis thalia

Scoring table:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; dihydropyrimidine dehydrogenase; DPD; slicing defect; detection; 5-fluorouracil; cancer; anticancer; uraciluria; ds
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AAX20311
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AAX20264
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/note= "Encodes
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P-PSDB; AAW30092.
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Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                  A novel method has been developed for detecting the splicing defect in the dihydropyrimidine dehydrogenase (DPD) gene. The method comprises determining whether genomic DNA containing the DPD gene has a wild-type intron-exon boundary for an exon that encodes amino acids (aa) 581-635 of the corresponding DPD protein. The present sequence represents a DPD genomic fragment which encodes the amino acids 581-635. The method is used specifically to determine sensitivity of subjects to the anticancer agent 5-fluorouracil, which is dangerously toxic to those with DPD defects. It can also be used to diagnose DPD-deficiency disorders such as uraciluria.
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                                                            Disclosure; Fig 1; 38pp; English
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gene - used
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                                                                                                                                                                                                                                                                                                                             DPD; dihydropyrimidine-dehydrogenase; monoclónal antibody; immunoassay reagent; cancer patient; treatment; antitumour 5-fluorouracil; affinity purification; toxicity; ss.
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93.8%; Pred. No. 1.5e
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The DPD gene, DPYD, is located at chromosome 1p22. The cDNA can be inserted into a vector and used for prodn. of DPD (AAR91420) in transformed host cells, or used as a selectable marker that functions in prokaryotic and eukaryotic cells. It can also be utilised as a probe to detect DPD deficiency in an individual, i.e. to identify risk of toxic reaction to 4-fluorouracil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bovine; liver; human; dihydropyrimidine dehydrogenase; DPD; pyrimidine catabolism; 5,6-dihydropyrimidine; pyrimidine analogue; fluoropyrimidine; anticancer drug; 5-fluorouracil; FUTa; cancer; frameshift mutation; ss.
                                                                                                                                                                                                                                                                                  304 GGGAACCACCTCTGGCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCT
                                                                                                                                                                                                                                                                                                                                              CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTT
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                                                                                                                                                         Length 3957;
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                                                                                                                                                        19.9%; Score 171.2; DB 1'93.2%; Pred. No. 3.4e-29; ive 0; Mismatches 13.
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/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAT03133 standard; DNA; 4368 BP.
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                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                          CCCAGACAACaT 435
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                                                                                                                                                                         Similarity
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Best Local S
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                            1857 gggaaccacctctggccccatgtatggccctggacaaagctcctttctgaatattgagct 1916
                                                                                                                                                                                                                                                                                                                          Dihydropyrimidine dehydrogenase; DPD; DPYD gene; probe; deficiency; 5-fluorouracil; cytostatic; cancer; selectable marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pig and human di:hydro:pyrimidine dehydrogenase (DPD) genes and probes - useful for detection of DPD deficiencies and identification of humans at risk of toxic reaction to 5-fluoro:uracil anti-cancer treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human dihydropyrmidine dehydrogenase (DPD) cDNA (AAT14077) was isolated as 3 overlapping fragments obtd. from human liver cDNA libraries screened using pig DPD cDNA (see also AAT14077).
                                                                                                                                                                                                                                                                                             Human dihydropyrimidine dehydrogenase cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (2424..2447)
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/note= "primer RTR4"
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/note= "primer RTF1"
1536..1558
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/note= "primer RTR1"
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/note= "primer RTR5"
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/note= "primer RTR5"
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88..3165
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note= "primer H13"
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                                                                                                           Fernandez-Salguero P,
                                                                                           CCCAGACAACaT 435
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      dihydropyrimidine dehydrogenase (DPD). DPD catalyses the initial and rate limiting step in pyrimidine catabolism, the reduction of pyrimidines to 5.6-dihydropyrimidines. DPD is a complex enzyme consisting of two identical subunits, containing FWN. FAD and ironsulphur centers, and utilising NADPH as a cofactor. DPD has also been shown to catalyse the reduction of various pyrimidine analogues including the fluoropyrimidine anticancer drug 5-fluorouracil (FUra). Up to 85% of administered FUTA may be used in the detection of DPD in a sample, esp isolated from a cancer patient. According to the amount of DPD detected, a therapeutically effective amount of FUTA may be determined and administered. DPD deficiency, leading to life-threatening toxicity on exposure to FUTA, in a human caused by a frameshift mutation may be determined by means of a molecular biological assay to detect the deletion of an A residue at codon 318 within the
                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                               1764 caccaaaactttctctcttgataaggacattgtgacaatgtttcccccagaatcatccg 1823
                                                                                                                                                                                                                                                                                                                                                                                               1824 gggaaccacctctggccccatgtatggccctggacaaagctcctttctgaatattgagct 1883
                                                                                                                                                                                                                                                                                                                                                                                                                                     1884 catcagtgagaaaacggctgcatattggtgtcaaagtgtcactgaactaaaggctgactt 1943
                                                                                                                                                                                                                                                                                                                        244 CTCAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCCATAATCATCCG 303
                                                                                                                                                                                                                                                                                                                                                                                                                       364 CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTT 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bovine; liver; human; dihydropyrimidine dehydrogenase; DPD; pyrimidine catabolism; 5,6-dihydropyrimidine; pyrimidine analogue; fluoropyrimidine; anticancer drug; 5-fluorouracil; FUra; cancer;
                                                                                                                                                                                                                                                                                                                                                                        GGGAACCACCTCTGGCCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCT
                                                                                                                                                                                                                                                                                                                                                                                    Length 4368;
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 sequence represents the DNA sequence encoding human
                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                    Sequence 4368 BP; 1325 A; 829 C; 932 G; 1282 T; 0 other;
                                                                                                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                       Score 171.2; DB 1
Pred. No. 3.5e-29;
0; Mismatches 13
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/product= Human lymphocyte DPD
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                                                                                                                                                                                                                                                                     19.9%;
93.2%;
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1260..1288
/*tag= d
3117..3139
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/*tag= 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424 CCCAGACAACaT 435
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Best Local Similarity
                                                                                                                                                                                                             DPD-coding region.
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pyrimidine dehydrogenase (DPD). This sequence was amplified using the primer sequences given in AAT03144-47. DPD catalyses the initial and rate limiting step in pyrimidines catabolism, the reduction of pyrimidines to 5/6-dihydropyrimidines. DPD is a complex enzyme consisting of two identical subunits, containing FMN, FAD and ironsulphur centers, and utilising NADPH as a cofactor. DPD has also been shown to catalyse the reduction of various pyrimidine analogues. Up to 81% of administered FUR as a catabolised by DPD, and it therefore governs the effectiveness of FUR as an anticancer drug. DPD genes or fragments of them may be used in the detection of DPD in a sample, esp. isolated from a cancer patient. According to the amount of DPD detected, a therapeutically effective amount of FUR and administered. DPD deficiency, leading to life. Chreatening toxicity on exposure to FUR's, in a human caused by a frameshift mutation may be determined by means of a molecular biological assay to detect the deletion of an A residue at codon 318 within the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the cDNA sequence encoding human dihydro-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel di:hydro:pyrimidine dehydrogenase gene - used to optimise 5-fluoro:uracil doses given to cancer patients
/note= "Position of single base deletion in DPD
deficient patients"
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Pred. No. 3.5e-29;
0; Mismatches 13; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                               Lu Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 7; 207pp; English.
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93.28;
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Best Local Similarity 93.2*
Matches 179; Conservative
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                                                                                                                                                                                                             Bovine dihydropyrimidine dehydrogenase cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                            /product= Bovine DPD complement (2032..2051)
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57..3144
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Primer D"
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/note= "Primer B"
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/note= "Primer C"
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/note= "Primer A"
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/note= "Primer
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                                             1965 cagacaatat 1974
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                 426 CAGACAACAT
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                                                                                                                                                                                                                                                                                                                   Bos taurus
                                                                                                                                                   AAT03142;
                                                                                                        AAT03142
                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dihydropyrinidine dehydrogense (DDD). DDD catalyses the initial and rate limiting step in pyrimidine catabolism, the reduction of pyrimidines to 5.6-dihydropyrimidines. DPD is a complex energine consisting of two identical subunits, containing FMN. FAD and ironsulphur centers, and utilising NADPH as a cofactor. DPD has also been shown to catalyse the reduction of various pyrimidine analogues including the fluoropyrimidine anticancer drug 5-fluorouracil (FUra). Up to 85% of administered FUra may be catabolised by DPD, and it therefore governs the effectiveness of FUra as an anticancer drug. DPD genes or fragments of them may be used in the detection of DPD in a sample, esp. isolated from a cancer patient. According to the amount of DPD detected, a therapeutically effective amount of FUra may be theratening toxicity on exposure to FUra, in a human caused by a frameshift mutation may be determined at codon 318 within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                         Bovine; liver; human; dihydropyrimidine dehydrogenase; DPD; pyrimidine catabolism; 5,6-dihydropyrimidine; pyrimidine analogue; fluoropyrimidine; anticancer drug; 5-fluorouracil; FUra; cancer; frameshift mutation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel di: hydro: pyrimidine dehydrogenase gene - used to optimise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents the DNA sequence encoding bovine liver
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                                                                                                                                                                                                                                                                                                                                                                                            Zhang R;
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Pred. No. 1.5e-25;
0; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5-fluoro:uracil doses given to cancer patients
                             Bovine dihydropyrimidine dehydrogenase gene.
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88.4%;
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Best Local Similarity
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04-JUN-1996
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                                                                                                                                    Bos taurus.
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This sequence represents the cDNA sequence encoding bovine liver dihydropyrimidine dehydrogenase (DPD). This sequence was isolated using the primers given in AAT03134-41 and AAT14638. DPD catalyses the initial and rate limiting step in pyrimidine catabolism, the reduction of pyrimidines to 5,6-dihydropyrimidines. DPD is a complex enzyme consisting of two identical subunits, containing FMN, FAD and iron-
Bovine; liver; human; dihydropyrimidine dehydrogenase; DPD; pyrimidine catabolism; 5,6'dihydropyrimidine; pyrimidine analogue; fluoropyrimidine; anticancer drug; 5-fluorouracil; FUra; cancer; frameshift mutation; ss.
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                                            therefore governs the effectiveness of Fura as an anticancer drug.
DPD genes or fragments of them may be used in the detection of DPD in a sample, esp. isolated from a cancer patient. According to the amount of DPD detected, a therapeutically effective amount of FUra may be determined and administered. DPD deficiency, leading to life-threatening toxicity on exposure to FUra, in a human caused by a frameshift mutation may be determined by means of a molecular biological assay to detect the deletion of an A residue at codon 318 within the
  DPD has also been
                                                                                                                                                                                                                                                                                    ccaaaactttctctcttgataaggatatagtgacaaatgtttcacccagaatcatccggg 1843
                                                                                                                                                                                                                                                                                                                                                                          Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
sulphur centers, and utilising NADPH as a cofactor. DPD has also beer shown to catalyse the reduction of various pyrimidine analogues including the fluoropyrimidine anticancer drug 5-fluorouracil (FUra). Up to 85% of administered FUra may be catabolised by DPD, and it
                                                                                                                                                                                                                                                            246 CAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCCATAATCATCGGG 305
                                                                                                                                                                                                                                                                                                             GAACCACCTCTGGCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCA 365
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                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                          Length 4430;
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Pred. No. 1.5e-25;
0; Mismatches 22; Indels
                                                                                                                                                                        Sequence 4430 BP; 1333 A; 871 C; 955 G; 1271 T; 0 other;
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88.4%;
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17-MAR-2000; 2000US-0190259.
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Matches 168; Conservative
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                                                                                                                                                  DPD-coding region.
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present invention relates to a composition comprising two nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 ATTTAATGTATATAAAATTCCTCTGCAAATATGTGAGGGGGGCGCCTCATAAATATTG 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309 CCACCTCTGGCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCATCA 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        369 GTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCCCAG 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches)
                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                      Length 936;
                                                                                                      and single-nucleotide polymorphisms, e.g. for genotyping monitoring gene expression.
                                                                                                                                                                                                                                                                                                         DB 22;
                                                                                                                                                                                                         Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                                                                                                                                                                                                                                                                                         Query Match
17.78; Score 1.08; Best Local Similarity 1.08; Pred. No. 3.4e-25;
Matches 8; Conservative 512; Mismatches 271;
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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        GTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCCCAG 428
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17-MAR-2000; 2000US-0190259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention relates to a composition comprising two nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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17-MAR-2000; 2000US-0190259.
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and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                   8; Conservative 512; Mismatches 271; Indels
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Pred. No. 3.4e-25;
                         Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other,
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Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 AAGATAAATATTTTTTTTTTTTTTCGCTGTTCTAAACCTAGGGTTACAAGAAGTAATTTATC 68
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                                                                                                                       ETM; mismatch; genotyping;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CLIN-) CLINICAL MICRO SENSORS INC
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                                                        Oligonucleotide D2004
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TACATAAGCAGAAGGAAGAAATGAAATACTCATTTTATTGAGTTGGCCCCCCACTGTAT 728
                                                                                                                                                                                                                                                                     GTGGCTGGTATTTATGAAGGTGATGACCCAGGAAGAAATTGTAAAACTATAAACCACTCCA 788
                                                                                                                                                                                                                                          present invention relates to a composition comprising two nucleic
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                                                                                                                                                                         AAACCCACACAATGTGAAGCTCTGTTATAAATGGGTGCCATGTAAGATGGAAGAAGTATC
                                        TITAAACATCCAATICATAGGCITATAAATATTAATGTGTATATTTATCAACGAATCTG
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Pred. No. 3.4e-25;
2; Mismatches 271:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGAGCTAACAAATACTTTATTTTACCTTTTTTATTTGCAAGTAGTTTATGTTCAATTCTA 128
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                                                                                                                                                                        (CLIN-) CLINICAL MICRO SENSORS INC
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qene expression; ss
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GIGGCTGGTATTTATGAAGGTGATGACCCAGGAAGAAATTGTAAACTATAAACCACTCCA 788
                                                                                                                                                                                                                                                                                                                                                               Dihydropyrimidine dehydrogenase; DPD; DPYD gene; probe; deficiency; 5-fluorouracil; cytostatic; cancer; selectable marker; ss.
                                                                   AAACCCACACAATGTGAAGCTCTGTTATAAATGGGTGCCATGTAAGATGGAAGAAGTATC
                                                                                                                                                                                                                     602 wwwwwwwwwwwwwwwwwwwwwwwwwwwwww
                                                                                                                                                                                                                                                                                            TACATAAGCAGAAGGAAGAGAATGAATACTCATTTTATTGAGTTGGCCCCCCAGTAT
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probes - useful for detection of DPD deficiencies and
identification of humans at risk of toxic reaction to
5-fluoro:uracil anti-cancer treatment
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                                                                                                        246 CAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCATAATCATCCGGG 305
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                                                                                                                                                         GAACCACCTCTGGCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCA 365
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                                                          Score 151.6; DB 17; Length 4447;
Pred. No. 7.9e-25;
0; Mismatches 24; Indels 0;
                        Sequence 4447 BP; 1285 A; 928 C; 1000 G; 1234 T; 0 other;
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gene expression; ss.
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                                                          17.6%;
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                                                          Query Match 17.69
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.

Email: cgapbs-r@mail.nih.gov Tissue Procurement: Louis Staudt, M.D., Ph.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	DNA Sequencing by: Incyte Genomics, Inc.			/lab_host="DHLDB" (phage-resistant)" /lab_host="DHLDB" (phage-resistant)" /note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally; oligo-dT primed. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technologies.	Note: this is a NIH_MGC Library." BASE COUNT 222 a 234 c 253 g 229 t ORIGIN	Query Match 19.9%; Score 171.2; DB 172; Length 938; Best Local Similarity 93.2%; Pred. No. 4.4e-29; Matches 179; Conservative 0; Mismatches 13; Indels 0; Gaps 0;	Qy 244 CTCAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTCCCCCATAATCATCCG 303 	QY 304 GGGAACCACCTCTGGCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCT 363 	Qy 364 CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTT 423 	Qy 424 CCCAGACAT 435                 Db 440 TCCAGACACAT 451	RESULT 2 CNSO2EEL/C CNSO2EEL 853 bp DNA GSS 13-MAY-2000 LOCUS DEFINITION Tetrandon nigrovitridis genome survey sequence T7 end of Clone 252A0R of library G from petrandon nigrovitridis	ACCESSION AL193635. VERSION AL193635.1 GI:7831741 KEYWORDS GSS; genome survey sequence. SOURCE Tetraodon nigroviridis. ORGANISM Tetraodon nigroviridis. Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoceleostei;	Acanthomorpha; Acanthopteryg11; Percomorpha; Tetraodontilormes; Tetraodontidae; Tetraodon.  REFERENCE 1 (bases 1 to 833) AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and	TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis JOURNAL Unpublished REFERENCE 2 (bases 1 to 853) AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
	Description	BG024298 602274460 AL193635 Tetraodon AW018806 fd60003.y AL058798 Drosophil BE288474 601095732 AL063921 Drosophil	~~ 10 80 0		~ 10 10 -		AZ53554 ENTESPETA AL064580 Drosophil AZ534072 ENTERSTR AZ 34072 ENTERSTR				AZ690408 ENTLWOBTR AL206746 Tetraodon AZ683764 ENTL196TR AL069706 Drosophil	EST 24-JAN-2001 CDNA clone IMAGE:4362302 5',	a. Vartehrata. Filtalooctomi.	i; Hominidae
\$ Query	ore Match Length DB ID	1.2 19.9 938 172 BG024298 0.8 10.5 853 220 CNSOZEEI 7.8 10.2 621 110 AW018806 1.4 8.3 1207 219 CNSO0175 64 7.4 562 165 BE288474 58 6.7 1101 219 CNSO0396	6.4 500 107 6.4 483 151 6.1 1101 219 6.0 1301 219	6.0 6.0 868 6.0 881 6.0 899 6.0 898	6.0 1101 219 5.9 987 219 5.9 1025 219 5.9 1101 219	5.8 1101 219 5.8 632 107 5.8 947 247 5.8 1101 219 5.8 867 219	5.7 872 245 5.7 1101 219 5.7 896 245 5.7 816 245	5.6 872 245 5.6 329 105 5.6 911 248	5.6 898 247 5.6 987 219 5.6 1007 219	ับบบบบ รับบับบับ	5.5 909 248 5.5 1032 220 5.5 1048 248 5.5 1101 219	ALIGNMENTS 938 bp mRNA H_MGC_85 Homo sapiens	BG024238 BG024298.1 GI:12409730 EST. human. Homo sapiens Rukarvota: Metazoa. Chordata. Craniata.	Primates; nci.nih.gov of Health,

RESULT 1
BG024298
LOCUS
DEFINITION 6

ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

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www.rzpd.de)
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                                                                                                                            Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostcmi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Rasborinae; Danio.

(Chark, M., Danson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hiller, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., and Wilson, R., McCann, R., Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW018806 621 bp mRNA EST 13-SEP-1999
fd60d03.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to
SW:DPYD_HUMAN Q12882 DIHYDROPYRIMIDINE DEHYDROGENASE [NADP+]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
             Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                          /note="Genoscope sequence ID : COAG262BA04LP1-end : T7" 189~{\rm c} 136~{\rm g} 269~{\rm t} 7~{\rm others}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     258 TCTTTCATGAGGACATTGTGACAAATGTTTCCCCCATAATCATCGGGGGAACCACCTCTG 317
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 853;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 90.8; DB 220; Leuy-...
Pred. No. 1e-10;
                                                                                                                                                                                                                                                               /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="262A08"
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Unpublished (1998)
                                                                                                                                                                                                                         Location/Qualifiers
Saurin, W. and Weissenbach, J.
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                                                                                                                                                                                                                                                                                                                        /clone_lib="G
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67.9%;
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Direct Submission
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cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Mashington University Genome Sequencing Center Clone distribution: Genome Systems. St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome survey sequence TET3 end of BAC # 8ACC # BACR 3612 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                 /Lissue_type="26 somite embryos, adult livers, shield stage embryos" /lab_host="XLI-blue MRF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              275 GTGACAAATGTTTCCCCCATAATCATCGGGGAACCACCTCTGGCCCCATGTATGGCCCT 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    335 GGACAAAGCTCCTTTCTGAATATTGAGCTCATCAGTGAGAAAACGGCTGCATATTGGTGT 394
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1207)
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                                                                                                                                                                                                                                                                                                                           /clone_lib="Zebrafish WashU MPIMG EST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     395 CAAAGTGTCACTGAACTAAAGGCTGACTTCCCAGACAACATAA 437
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                                                                                                                                                                                                                                                                           /organism="Danio rerio"
/db_xref="taxon:7955"
                                                                                                                                                                                   Seg primer: T3 ET from Amersham
High quality sequence stop: 491.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                              /sex="mixed"
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Web: www.genoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDCP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDCP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
Pl and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                                                                                                                                                                                                                             /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unddirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster genome survey sequence TET3 end of BAC # BACROBK10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.

AL063921
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.4%; Score 64; DB 165; Length 562;
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/db_xref="taxon:7227"
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                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:3490423"
/clone_lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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  column: 08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135
                                                                                                            /organism="Mus musculus"
                         High quality sequence stop: 562.
Location/Qualifiers
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                                                                                                                                         /strain="C57/B6"
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  Plate: LLAM8532
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                                                                                                 - Web: www.genoscope.cns.fr)

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and bow to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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                      Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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NIH-MGC http://mgc.nci.nih.gov/.
National institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    327 ATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCATCAGTGAGAAAACGGCTGCAT 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              267 AGGACATTGTGACAAATGTTTCCCCCATAATCATCCGGGGGAACCACCTCTGGCCCCATGT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399 AGGATCTGGTCACGAATGTCTCGCCGCGATCGTCAGGGGCACCACGTCGGGCTACAAGT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="texon:7227"
/clone_lib="RPCT-98"
/clone="BACR03G12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 71.4; DB 21 Pred. No. 2.8e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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Best Local Similarity 63.9%;
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BE288474
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FORWARD: AGGAAACAGCTATGACCAT
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81-3-5449-5410
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   rel:
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 500)
Watanabe,J., Sasaki,M., Suzuki,Y. and Sugano,S.
FULL-malaria: a datebase for a full-length enriched cDNA library from human malaria parasite, Plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AU086287 500 bp mRNA EST 27-JAN-2001 AU086287 Sugano Malaria cDNA library Plasmodium falciparum cDNA clone XPFn2249, mRNA sequence.
                                                                                                                                                                                                           70 GGAGCTAACAAATACTTTATTTTACCTTTTTATTTGCAAGTAGTTTATGTTCAATTCTAA 129
                                                                                                                                                                                                                                 130 TTTAATGTATATAAAAATTCCTCTGCAAATATGTGAGGAGGGACCTCATAAAATATTGT 189
                                                                                                                                                                                                                                                                                                                                                                190 CATATGGAAATGAGCAGATAATAAGATTATAGCTTTTCTTTGTCAAAAGGAGACTCAAT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 ATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCATAATCATCCGGGGAAC 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 CACCTCTGGCCCCATGTATGGCCCTGGACAAGCTCCTTTCTGAATATTGAGCTCATCAG 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               370 TGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCCCAGA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   691 МСМСТИТСИНСҮҮҮҮННҮТАНИТНТИНЖАНҮҮММҮҮММАҮҮММ------УСТАСТҮНҮН 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         430 CAACaTAAGTGTGATAAAAATCTAAAAGAAGAAATTGGCATAAGTTGGTGAATGTTTAT 489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   490 TTAAACATCCAATTCATAGGCTTATAAATATTAATGTGTATATTTTATCAACGAATCTGC 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| : [:::::|| |:|:|::::|| 805 YICCYMCWHYYHTWWHHTTTHWAWHTHTWCWWW 864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                          511 ИТТААВМАААААААВАВАВМААВМАТАВАТИТИТИТУТТИВАМАТАВАМСМАВИ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                571 ҮҮНТҮГТҮТҮНҮХТҮМТҮТМТИНҮНТМҮТНАМАНТТИҮНИҮНГҮАММНИМТИНИТМИАМ
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                                                                                                                               6.7%; Score 58; DB 219; Length 1101; 20.4%; Pred. No. 0.0032; Live 216; Mismatches 232; Indels 6
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The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                                         others
                                                       503
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                                                       202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : |: : :::: | | |::: | 925 MTCHWMWHMHWHWHWHMMATWMTTMTTMMM 954
/clone_lib="RPCI-98"
/clone="BACR08K10"
/note="end : TET3"
a 64 c 131 9
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Contact: Junichi Watanabe
                                                                                                                                                   Best Local Similarity 20.4%; Promatches 116; Conservative 216;
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                                                                                                                                   Query Match
                                                     BASE COUNT
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COMMENT
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Email: jwatanab@nanage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).
Location/Qualifiers
1. 500
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Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid,
W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cDNA libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 TCTGGAGCTAACAATACTTTATTTTACCTTTTTATTTGCAAGTAGTTTATGTTCAATTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127 TAATTTAATGTATATTAAAAATTCCTCTGCAAATATGTGAGGAGGGACCTCATAAAATAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    322 AAATAAAATCCATATATATATATATATAAATAAAACATTTTATAAATAAATATAAAAAT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 TGAAGATAAATATTTTTGTTTTTGCTGTTCTAAACCTAGGGTTACAAGAAGTAATTTA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    187 TGTCATATGGAAATGAGCAGATAATAAAGATTATAGCTTTTCTTTGTCAAAAGGAGAGACTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 500
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                                                                                                                                                                                                                                                                                                                                              others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                         /clone="xPFn2249"
/clone_lib="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
/ 25 c 24 g 231 t 6 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov
                                                                                                                                                                          /organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 AATATCTTTACTCTTTCATGAGGACATTGTGACAAA, 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0.015;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     442 ATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATAAA 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55;
                                                                                                                                                                                                    /strain="3D7"
/db_xref="taxon:5833"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
Eukaryota, Metazoa, Chordata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF653737
BF653737.1 GI:11918869
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.48;
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Gaps

Length 1101;

others

232

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FEATURES

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/db_xref="taxon:5759"
/clone_lib="Entamoceba histolytica Sheared DNA"
/clone_lib="Entamoceba histolytica Sheared DNA"
/clone_lib="Entamoceba histolytica Structed at The Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (L.S. (1993) Entamoceba histolytica: a method for isolate identification. Exp. Parasitol.
77.450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ527678 912 bp DNA GSS 03-NOV-2000
ENTBN23TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 912)

1.oftus, B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
                                                                                                                                                                                                                                                                                                                          61 AATTTATCTGGAGCTAACAAATACTTTATTTTACCTTTTTATTTGCAAGTAGTTTATGTT 120
                                                                                                                                                                                                                                                                                                                                                         121 CAATICTAATITAATGIATATTAAAAATTCCTCTGCAAATATGTGAGGAGGGACCTCATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AAATATTGTCATATGGAAATGAGCAGATAATAAAGATTATAGCTTTTCTTTGTCAAAAGG 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       723 ТАТИТАТИМАТИТТИТТТТТТТТТТТТТТТТТТТТТААТТТТААТТТААТТАИММААТ 664
                                                                                                                                                                                                                   1 TGTTAATGAAGATAAATATTTTTTTTTTTTTTCGCTGTTCTAAACCTAGGGTTACAAGAAGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 603 AATWAWATTTATAWATTAATATAWWTTWTAAATTWTTAATWTATWWTTTAAATTATWTT
                                                                                                 6.1%; Score 22...
35.7%; Pred. No. 0.055;
+ive 51; Mismatches 127; Indels
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/organism="Entamoeba histolytica"
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Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
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AZ527678.1 GI:11079801
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Direct Submission

AL SUBMISSION

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazucoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Carlitute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: on bw sp, the same strain used for the BDGP's pl and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

Location/Qualifiers
                                                                                              1..483
/organism="Bos taurus"
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/tissue_type="pooled"
/lab_host="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Inbrary made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."

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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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Pred. No. 0.017;
0; Mismatches 7; Indels
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/db_xref="texon:7227"
/clone_lib="RPCI-98"
/clone="BACR29B23"
                           Plate: 70 row: B column: 4
Seg primer: ATTTAGGTGACACTATAG.
BACKWARD: GTTTTCCCAGTCACGACG
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Best Local Similarity 89.7
Matches 70; Conservative
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Oscegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswall Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29F01 of RPCI-98 library from Drosophila melanogaster (fruit
H.O. and Venter, J.C. (Making small insert libraries whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and Barell, Oxford University Press, 1999)."
                                                                                                                                                                                                                                                                                                           481 AATGITTATTTAAACAICCAATICATAGGCITATAAATATTAATGIGTATATTTATCAA 540
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                                                                                                                                                       Score 52; DB 245;
Pred. No. 0.075;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fly), genomic survey sequence.
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/strain="HM1:IMSS"
/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pH051; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, c.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
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ENTFW05TF Entamoeba histolytica Sheared DNA Entamoeba histolytica
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                                                                                                                                                                                                                                                                                                                                                                                       61 AATTTATCTGGAGCTAACAAATACTTTATTTTACCTTTTTATTTGCAAGTAGTTTATGTT 120
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                                                                                                                                                               Length 1101;
                                                        214 others
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Contact: Brandan J Loftus

Contact: Brands J Loftus

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850,

Fax: 301 838 0208
                                                                                                                                                                                                                        44; Mismatches 136;
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Eukaryota; Entamoebidae; Entamoeba.
1 (bases 1 to 853)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences
HM1:IMSS sheared DNA library
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                                                        351
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High quality sequence stop: 838.
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/clone="BACR29P01"
/note="end : TET3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic, DNA sequence.
AZ548198
AZ548198.1 GI:11171567
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Seg primer: M13-Forward
                                                                                                                                                                  6.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Entamoeba histolytica.
                                                                                                                                                                                                                        Matches 107; Conservative
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tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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/note="Vector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
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Eukaryota: Entamoebidae; Entamoeba.

E 1 (bases 1 to 868)

S Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library

L Unpublished (2000)

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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
Seq primer: M13-Reverse
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ENTJ141TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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0
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                                                                                                                                                                                                                                      Score 51.8; DB 245; Length
Pred. No. 0.083;
0; Mismatches 127; Indels

    .868
    /organism="Entamoeba histolytica"

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High quality sequence stop: 779
Location/Qualifiers
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AZ686179
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Matches 128; Conservative
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VERSION
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TITLE
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SOURCE
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using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
DNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AZ681140 881 bp DNA GSS 14-DEC-2000
ENTMC34TR Entamoceba histolytica Sheared DNA Entamoceba histolytica
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Eukaryota; Entamoebidae; Entamoeba.
I (bases 1 to 881)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
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50.2%; Pred. No. 0.083;
tive 0; Mismatches 127;
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/strain="HM1:IMSS"
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Contact: Brendan J Loftus
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The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
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Fax: 301 838 0208
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AZ681140
AZ681140.1 GI:11818286
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ORIGIN
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VERSION
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TITLE
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Search completed: November 20, 2001, 16:21:54
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHOS1; Site_1: Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark,
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ENTCX21TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
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1 (bases 1 to 899)
Loftus,B., Van Aken,S. and Fraser,C.
Determination of clone end sequences from Entamoeba histolytica
HMI:HMS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Class: shotgun
High quality sequence start: 93
High quality sequence stop: 858
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AZ542627.1 GI:11160786
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Entamoeba histolytica
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Matches 128; Conservative
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ORIGIN
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TITLE
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AZ542627
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/note="Vector: pHOSI; Site__1: Bit I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of E. histolytica using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. Exp. Parasitol. 77:450.) The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 GTTGATTTATTTTAATATTTTGTTCAACATAAATTCAATAAAACATATATTTTGATAATAT 490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         504 CATAGGCTTATAAATATTAATGTGTATATTTTATCAACGAATCTGCCAGTTGCTTTGCTG
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0
                            /strain="HM1:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 51.8; DB 245; Length 899;
Pred. No. 0.083;
0; Mismatches 127; Indels 0;
/organism="Entamoeba histolytica"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6.0%;
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Best Local Similarity
Matches 128; Conserv
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Run on:

em\_ov:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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HSU57655
HSDYPDGEN
HSU09178
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AB003063
HSU20938
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gb_htg23:*
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gb_htg9:*
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9b_htg16:
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9b_htg18:
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                                                                                  (without alignments) 9046.205 Million cell updates/sec
                                                                      Search time 1472.19 Seconds
                                                                                                                                              1 TGTTAATGAAGATAAATATT......AGTGGGAAATAATTTATTAA 861
                                                                                                                                                                                                                                    2688314
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                          1344157 seqs, 7733874588 residues
                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                      November 20, 2001, 14:27:41;
                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                              OM nucleic - nucleic search, using sw model
                                                                                                                                                                      IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_htg_inv2:*
em_htg_other:*
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Perfect score:
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AL356574 Homo sapi U57655 Human dihyd X95670 H.sapiens D U09178 Human dihyd AR027740 Sequence AB003063 Homo sapi U20938 Human lymph U20981 Bos taurus

Description

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                                                                                                              AL445207 Human DNA
AC026816 Homo sapi
AC021276 Homo sapi
AC025645 Homo sapi
AC025645 Homo sapi
AF065298 Arabidops
AL162723 Homo sapi
AF044859 Eurema da
AF004112 Plasmodiu
K00907 paramecium
                                                                 AL122025 Drosophil
AC044793 Homo sapi
AC04153 Plasmodiu
AC010228 Homo sapi
X04775 Dictyosteli
                    D85035 Rattus norv
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166494 Sequence 14
                                       AC014157 Drosophil
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AC016700 Homo sapi
AP002529 Homo sapi
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                                               AE003446 Drosophil
J65491 Drosophila
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AF030694 Plasmodiu
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ENKARYOGI, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Manmalla, Eutheria; Primates; Catarrhini, Hominidae, Homo.
1. (bases 1 to 180286)
                            Caenorhabdi
                                                                                                                                                                                                                         paramecium
                                                                                                                                                                                                                                 paramecium
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 U09179 Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
Submitted (20-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
requests: clonerequest@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                          AL356574 180286 bp DNA HTG 23-JAN-2001
Homo sapiens chromosome 1 clone RP11-359C24, *** SEQUENCING IN
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                                                                                                                                                                                                                      K00911
K00906
K00904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid: L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 166105 bases at least 040
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PARMTDI4H
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PARMTDI4A
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166494
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AP000794
AC025645
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AC010228
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AC026816
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AF044859
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AC060784
AC027625
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AP002529
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AC004482
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                                               AE003446
DMU65491
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           AR027741
D85035
                             CELC25F6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
150.2
150.2
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70.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
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Consensus quality: 171672 bases at least Q30
Consensus quality: 174563 bases at least Q20
Insert size: 177786; sum-of-contigs
Insert size: 186027; 5.1% error; agarose-fp
Quality coverage: 3.18x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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100 bp
f 3486 bp in length.
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100 bp in length
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38453: contig of 11587 bp in length
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111029: contig of 12729 bp in length
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15191 23545: contig of 8355 bp in length
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26766: contig of 3121 bp in length
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51984: contig of 6006 bp in length
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58204: contig of 6120 bp in length
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5117 bp in length
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contig of 3608 bp in length
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contig of 3837 bp in length
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/db_xref="taxon:9606"
/chromosome="l"
/clone="RR11-159C24"
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160091 163742; contig of 36
163743 166322; contig of 24
163843 166322; contig of 24
166323 166422; gap of 16
166423 176700; contig of 16
176701 176800; gap of
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121093: contig of
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141587 146703: contig of
146704 146803: gap of
146804 149034: contig of
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141486: contig of
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159990: contig of
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45878: con+
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3; 50067 49887 50187 50127 50007 49947 49827 49767 49707 49706 TCACTGTATGTGGCTGGTATTTATGAAGGTGATGACCTTAGGAAGAAATTGTAAACTATA 49647 240 120 629 360 420 479 539 599 719 778 837 dehydrogenase (DPYD) gene, partial cds Gaps 9 01-SEP-1996 1 TGTTAATGAAGATAAATATTTTTTTTTTTTCGCTGTTCTAAACCTAGGGTTACAAGAAGT AATTTATCTGGAGCTAACAAATACTTTATTTTACCTTTTTATTTGCAAGTAGTTTATGTT 50066 GCTCATCACTGAGAAAACGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGA CCGGGGAACCACCTCTGGCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGA 480 GAATGTTTAAACATCCAATTCATAGGCTTATAAATATTAAATGTGTATATTTATCA CCACTGTATGTGGCTGGTATTTATGAAGGTGATGACC-CAGGAAGAAATTGTAAACTATA 361 GCTCATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGA 421 CTTCCCAGACAAGGTAAGTGTGA-TAAAAATCTAAAACAAGAGAATTGGCATAAGTTGGT 779 AACCACTCCAAATATAAACCCGAGGCAGAAGCAGCATATC-TCCTATGAAGCCTGTATTT Length 180286 Indels DB 80; 90.0%; Score 775.2; DB 80 95.8%; Pred. No. 2.1e-142; 0; Mismatches TTTCAGTGGGAAATAATTTATTAA 49563 838 ACTCAGTGGGAAATAATTATTAA 861 HSU57655 626 bp Human dihydropyrimidine U57655 U57655.1 GI:1518606 Conservative Local Similarity hes 828; Conserv human Query Match DEFINITION ACCESSION VERSION KEYWORDS SOURCE Best Loca Matches 50246 720 61 181 49586 301 RESULT HSU57655 LOCUS Ω δ ŏ g δλ qq Qγ g δλ Dp δy g δ g ò qq Qγ q òγ οq οy q Qy OD οy qq qq Dp ò δ

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MD 20892, USA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                               Fernandez-Salguero, P.M., Wei, X., Jones, S., Idle, J.R. and
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                                                                             Gonzalez, F.J.
Lack of dihydropyrimidine dehydrogenase activity and thymine-uraciluria caused by a common splice mutation Hum. Mutat. (1996) In press
2 (bases 1 to 626)
                                                                                                                                               2 (bases 1 to oco,
Pernandez-Salguero,P.
Pernandez-Salguero,P.
Submitsted (07-MAY-1996) Pedro M. Fernandez-Salguero, J
Institutes of Health, 9000 Rockville Pike, Bethesda,
Location/Qualifiers
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Pred. No. 9.2e-110;
0; Mismatches 4;
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Matches 622; Conservative
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Vreken, P., Van Kullenburg, A.B., Meinsma, R., Smit, G.P., Bakker, H.D. De Abreu, R.A. and van Gennip, A.H.
A point mutation in an invariant splice donor site leads to exon skipping in two unrelated Dutch patients with dihydropyrimidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (14-FEB-1996) P. Vreken, Academic Med.Center, Univ.of Submitted (14-FEB-1996) P. Vreken, Academic Med.Center, Univ.of Amsterdam, Dep of Pediatrics and Clinical Chemistry, F0-224, P.O. Box 22700, NL-1100 DE Amsterdam, NETHERLANDS
Related sequences:
Meinsma et al, DNA Cell Biol. 14:1-6 (1995), U20938, and Yokota H et al, J. Biol. Chem. 269:23196 (1994).
                   17-FEB-1997
                                                                                                                                                                                                                                                       dihydropyrimidine dehydrogenase; DYPD gene; exon X; mutation.
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J. Inherit. Metab. Dis. 19 (5), 645-654 (1996)
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/product="dihydropyrimidine dehydrogenase"
/product="dihydropyrimidine dehydrogenase"
/protein_id="AaA57474.1"
/db_xref="G1:S89305"
/translation="MAPVLSKDSADIESILALNPRTQTHATLCSTSAKKLDKKHWKRN
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                                                                                                                              Dupuis, A., Skehel, J.M. and Walker, J.E.
A homologue of a nuclear-coded iron-sulfur protein subunit of
bovine mitochondrial complex I is encoded in chloroplast genomes
biochemistry 30 (11), 2954-2960 (1991)
       Mechanism-based inactivation of dihydropyrimidine dehydrogenase
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/citation=[5]
/function="catalytic cofactor NADPH/NADP binding site"
1492. .1524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /citation=[2]
/function="electron transfer center, FAD binding site"
2062. 2175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (22-APR-1994) Frank J. Gonzalez, National Cancer Institute, National Institutes of Health, 9000 Rockville Pike, Bethesda, MD 20892, USA Location/Qualifiers
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1117 t
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                                                                                                                                                                                                                                                                                 Wierenga, R.K., De Maeyer, M.C.H. and Hol, W.G.J.
Interaction of pyrophosphatase moieties with alfa-helixes
dincleotide binding proteins
Biochemistry 24, 1346-1357 (1985)
6 (Dass 1 to 3951)
Gonzalez, F.J.
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Pred. No. 4.2e-24;
0; Mismatches 13; Indels
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/standard_name="iron-sulfur center"
                                                       l. Chem. 267 (8), 5236-5242 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/tissue_type="liver"
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785 c 896 q
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/citation=[3]
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Rubredoxin reductase of Pseudomonas oleovorans. Structural
relationship to other flavoprotein oxidoreductases based on one NAD
and two FAD fingerprints
J. Mol. Biol. 212 (1), 135-142 (1990)
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1 (bases 1 to 3951)
Yokota, H., Fernandez-Salguero, P., Furuya, H., Lin, K., McBride, O.W., Podschuu, B., Schnackerz, K.D. and Gonzalez, F.J.

CDNA. cloning and chromosome mapping of human dihydropyrimidine dehydrogenase, an enzyme associated with 5-fluorouracii toxicity and congenital thymine uraciluria

J. Biol. Chem. 269 (37), 23192-23196 (1994)
                                                                                                                                                                                                                                                                                                           CAATTCTAATTTAATGTATATAAAAATTCCTCTGCAAATATGTGAGGGGGGCCCTCATA 180
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Human dihydropyrimidine dehydrogenase mRNA, complete cds.
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     Length 854;
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Porter, D.J., Chestnut, W.G., Merrill, B.M. and Spector, T.
                                                       Indels
     DB 93;
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                       Pred. No. 3.5e-86;
; Mismatches 18
     Score 488.2;
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56.7%;
96.2%;
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Fkuushima,M., Nagayama,S., Kawaquchi,Y. and Watabe,T.
Sulcidal inactivation of human dihydropyrimidine dehydrogenase by
(B)-5-(2-bromoviny1)uracil derived from the antiviral, sorivudine
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Mammalia; Eutheria; Primates; Catarrhini, Hominidae; Homo.
                                         1857 GGGAACCACCICIGGCCCCAIGIAIGGCCCTGGACAAAGCICCIIICIGAAIAIIGAGCI 1916
                                                                                           1917 CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTT 1976
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             GGGAACCACCTCTGGCCCCATGTATGGCCCTGGACGAAGCTCCTTTCTGAATATTGAGCT
                                                                          CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTT
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Gonzalez, F.J. and Fernandez-Salguero, P.
Conzalez, P. muman and pig dihydropyrimidine dehydrogenase
Patent: US 5856454-A 1 05-JAN-1999;
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Homo sapiens male lymphocyte cDNA to mRNA.
Homo sapiens
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787 c 897 q
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1. .3957
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AR027740
AR027740.1 GI:5938560
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Unclassified.
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Ogura, K.
Direct Submission
Submitted (10-APR-1997) to the DDBJ/EMBL/GenBank databases.
Kenichiro Ogura, Tokyo University of Pharmacy and Life Science,
Department of Drug Metabolism and Molecular Toxicology; 1432-1
Horinouchi, Hachioji, Tokyo 192-0392, Japan
(E-mail:ogurak@ps.toyaku.ac.jp, Tel:+81-426-76-4518)
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Human lymphocyte dihydropyrimidine dehydrogenase mRNA, complete
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                     Erratum:[[published erratum appears in Cancer Lett 1998 Jun 19;128(2):229]]
2 (bases 1 to 3078)
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Pred. No. 8.6e-24;
0; Mismatches 14; Indels
Cancer Lett. 122 (1-2), 107-113 (1998)
                                                                                                                                                                                                                                         1. .3078
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="lymphocyte"
/sex="male"
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Best Local Similarity 92.7%;
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1 (bases 1 to 4421)
Lu.Z., Zhang, R. and Diasio, R.B.
Dihydropyrimidine dehydrogenase activity in human peripheral blood mononuclear cells and liver: population characteristics, newly identified deficient patients, and clinical implication in
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Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
Bovidae; Bovinae; Bos.
                                         BTU20981 4421 bp mRNA MAM 17-JAN-1997
Bos taurus liver dihydropyrimidine dehydrogenase mRNA, complete
                                                                                                                                                                          1937 CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTGAACTAAAGGCTGACTT 1996
      304 GGGAACCACCTCTGGCCCCATGTATGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCT 363
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Albin, N., Johnson, M.R. and Diasio, R.B.
cDNA cloning of bovine liver dihydropyrimidine dehydrogenase
DNA Seq. 6 (4), 243-250 (1996)
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Submitted (13-FEB-1995) Pharmacology/Toxicology, University of Alabama at Birmingham, 1670 University Blvd., Birmingham, AL
                                                                                                                                       364 CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5-fluorouracil chemotherapy
Cancer Res. 53 (22), 5433-5438 (1993)
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Johnson, M.R.
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U20981.1 GI:677950
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/Product="dlhydropyrimidine dehydrogenase"
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/db_xref="dl="aab51366.1"
/db_xref="dl="aab512"
/db_xref="dl="aab512
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VSHQKGKPVPRIAELMDKKLPSFGPYLEQRKKIIAENKIRLKEQNVAFSPLKRNCFIP
KRPIPTIKDVIGKALQYLGTFGELSNVEQVVAMIDEEMCINCGKCYMTCNDSGYQAIQ
                                                                                                                                                                                                                              Diasio, R.B., Beavers, T.L. and Carpenter, J.T. Familial deficiency of dihydropyrimidine dehydrogenase. Biochemical basis for familial pyrimidinemia and severe 5-fluorouracil-induced
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LMGLKSDGTPWPAVGIAKRTTYGGVSGTAIRPIALRAVTSIARALPGFPILATGGIDS
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                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 4409)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 (bases 1 to 4409)
Johnson, M.R., Albin, N., Shahinian, H. and Diasio, R.B.
Identification of a frameshift in the DNA coding for
dihydropyrimidine dehydrogenase (DPD) in a DPD deficient patient
exhibiting 5-fluorouracil toxicity
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Purification and characterization of dihydropyrimidine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dehydrogenase from human liver
J. Biol. Chem. 267 (24), 17102-17109 (1992)
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J. Clin. Invest. 81 (1), 47-51 (1988)
88087908
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102. 3179
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4 (bases 1 to 4409)
Johnson, M.R.
GI:1926407
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Cetartiodactyla; Ruminantía; Pecora; Bovoidea

of

Location/Qualifiers

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BDKNCFNCEKLENNFDDIKHTTLGERGALREMRCLKCADAPCQKSCPTNLDIKSFIT
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EVFKAMNIPQIRNPSLPPPEKMPEAYSAKIALLGAGPASISCASFLARLGYNDITIFE
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/db_xref="G1:677951"
                                                                                                    /note="dihydrothymine dehydrogenase;
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75. 3152
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1. .4421
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DB 97; Length 4409;

19.7%; Score 169.6; DB 97; llarity 92.7%; Pred. No. 8.5e-24; Conservative 0; Mismatches 14;

Query Match Best Local Similarity Matches 178; Conserv

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244 CTCAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCCATAATCATCCG 303

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FDPETHLPTVTDTCTGCTLCLSVCPIIDCIKMVSRTTPYEPKRGLPLAVNPVS"
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Rubredoxin reductase of Pseudomonas oleovorans. Structural
relationship to other flavoprotein oxidoreductases based on one NAD
and two FAD fingerprints
J. Mol. Biol. 212 (1), 135-142 (1990)
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Mechanism-based inactivation of dihydropyrimidine dehydrogenase by
5-ethynyluracil
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 4441)
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A homologue of a nuclear-coded iron-sulfur protein subunit of
bovine mitochondrial complex I is encoded in chloroplast genomes
Biochemistry 30 (11), 2954-2960 (1991)
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Sus scrofa dihydropyrimidine dehydrogenase mRNA, complete cds.
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Interaction of pyrophosphatase moieties with alfa-helixes
dinclectide binding proteins
Biochemistry 24, 1346-1357 (1985)
6 (bases 1 to 4441)
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4365020
                                                                                                                 DB 7;
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Pred. No. 1.3e-20;
0; Mismatches 21
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88.8%;
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PDKNCFHCEKLENNPGDIKHTTLGERGALREAMRCLKCADAPCQKSCPTHLDIKSFIT
SISNKNYYGAAKMIFSDNPLGLTCGMVCPTSDLCVGGCNLYATEEGSINIGGLQQFAS
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VIVLGAGDTAFDCATSALRCGARRVFLVFRKGFVNIRAVPEEVELAKEEKCEFLPFLS
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KQEYVGGLSTSEI PQFRLPYDVVNFEI ELMKDLGVK I I CGKSLSENEI TLNTLKEEGY
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Submitted (22-APR-1994) Frank J. Gonzalez, National Institutes of Health, National Cancer Institute, 9000 Rockville Pike, Bethesda, MD 20892, USA
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1492. 1524
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//standard_name="iron-sulfur center"
//standard_name="iron-sulfur center"
//citation=[4]
//function="catalytic cofactor [4Fe-4S] binding site"
//function="catalytic cofactor [4Fe-4S] binding site"
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/citation=[3]
/function="uracil (substrate) binding site"
                                                                                                                                                                                                                                                                                                                                        /product="dihydropyrimidine dehydrogenase"
/protein_id="AAA57475.1"
/db_xref="GI:558307"
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Best Local Similarity 87.7%; Pred. No. 5.4e-20;
Matches 164; Conservative 0; Mismatches 23
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Sequence 3 from patent US 5856454.
                                                                                                                                                                     /organism="Sus scrofa"
/db_xref="taxon:9823"
/tissue_type="liver"
82. .3159
                                                                                                           Location/Qualifiers
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TDKNCFICEKLENNFDDIKHTTLGERGALREAVRCLKCADAPCQKSCPTSLDIKSFIT
SIANKNYYGAAKLIFSDNPLGLTCGWVCPTSDLCVGGCNLHATEEGPINIGGLQQFAT
EVFRAMNIPQIRSPLLPPPEHWPEAYSAKIALFGAGRASISCASFLARLGYSDITIFE
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Wilson,R., Ainscough,R., Anderson,K., Baynes,C., Berks,M.,
Bonfield,J., Burton,J., Connell,M., Copsey,T., Cooper,J.,
Coulson,A., Craxton,M. Dear,S., Du,Z., Durbin,R., Favello,A.,
Fulton,L., Gardner,A., Green,P., Hawkins,T., Hillier,L., Jier,M.,
Latretille,P., Lightning,J., Lloyd,C., McMurray,A., Mortimore,B.,
O'Callaghan,M., Parsons,J., Percy,C., Rifken,L., Roopra,A.,
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                                                                                                                                                                                                                                                          /protein_id="BAA33218.1"
/db_xref="G1:3628593"
              /tissue_type="liver"
59. .3136
                                                                                                                                                                      /EC_number="1.3.1.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.9%;
85.3%;
                                                                                      /dene="DPD"
                                                                                                                                            /dene="DPD"
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Matches 162; Conservative
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Direct Submission
Submitted (01-MAY-1996) to the DDBJ/EMBL/GenBank databases.

Submitted (01-MAY-1996) to the DDBJ/EMBL/GenBank databases.

Masahiro Kimura, Kobe Gakuin University, Faculty of Nutrition; 518

Arise, Ikawadani-cho, Nishi-ku, Kobe, Hyogo 651-21, Japan

(Tel:078-974-1551(ex:3242), Fax:078-974-5689)

2 (bases 1 to 4358)
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DPD; dihydropyrimidine dehydrogenase.
Battus norvegicus (strain:Wistar) 7-d-old male liver cDNA to mRNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cloning of rat dihydropyrimidine dehydrogenase and correlation of its mRNA increase in the rat liver with age J. Nutr. Sci. Vitaminol. 44 (4), 537-546 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAACCACCTCTGGCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCA 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        366 TCAGTGAGAAAACGGCTGCATATTGGTGTAAAGTGTCACTGAACTAAAGGCTGACTTCC 425
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D85035 4358 bp mRNA ROD 19-SEP-19
Rattus norvegicus mRNA for dihydropyrimidine dehydrogenase,
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Kaneko,M. and Tamaki,N.
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                                                                                                                                                              1 (bases 1 to 4447)
Gonzalez,F.J. and Fernandez-Salguero,P.
CDNA for human and pig dihydropyrimidine dehydrogenase
Patent: US 5856454-A 3 05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 150.2; DB 9;
Pred. No. 5.4e-20;
0; Mismatches 23;
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/dev_stage="7-d-old"
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                         /organism="unknown"
930 c 1000 g
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Rattus norvegicus
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                       AR027741.1 GI:5938561
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87.7%;
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/protein_id="AAA80431.1"
/bc.xref="G1:104945"
/translation="MIGSRELSKILLVSCLIGVLGVADASSSMYARRTASERLMSII
RPRMPQNPEFRSSQKIQKSIQLNPNRALPCCKDESGGSICKNLRRTDIKLFTQKCQTE
PDFSLVVCCSSCSDAGISYRKRAQKQVFIFTILVI"
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/protein_id="AAA80432.1"
/db_xref="G1:1049457"
/translation="MONGDIADSQITASSSFDKQSVGPQNARLHSELASGAWCPKPQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPDGSRLDTLDFKDSMFEDSQ1YTESG1KRYGSWPANRRFRSAASPFEKNQMNNSW1G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HVYMDGNFDTTTPVIRVLDPPIVASRIRFVPSSKNTRTVCMRAEIHGCKHEGVTYYST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cambridge CB10 IRQ, England e-mail: Iw@nematode.wustl.edu and jes@sanger.ac.uk NEIGHBORING COSMID INFORMATION:
The 5' cosmid is C41A3, 1000 bp overlap; 3' end lies in a gap followed by the cosmid T23F2. Actual start of this cosmid is at base position 1 of CELC25F6; actual end is at base position 43803 of CELC25F6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    using
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               analysis, using
in preparation)
                                                                                                of
           Sonnhammer, E.,
Smaldon, N., Smith, A., Sonnhammer, E. orrv-Mieq, J., Thomas, K., Vaudin, M.,
    Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E. Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M., Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Whilkinson-Sproat, J. and Wohldman, P.
2.2 Mb of contiguous nucleotide sequence from chromosome III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(join(5095. .5215,5259. .5385,5443. .5535,
                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coding sequences below are predicted from computer the program Genefinder(P. Green and L. Hillier, \mathfrak m s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to protein tyrosine kinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(5095, .5656)
/gene="C25F6.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (30-00T-1995) Robert Waterston
                                                                                                                                                                                                                                                                                                                                                                                                                      Department of Genetics, Wasl
St. Louis, MO 63110, USA,
Sanger Centre, Hinxton Hall
                                                                                                                                                                                                                                  The sequence of C. elegans cosmid C25F6
Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                   Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6128)
                                                                                                                                  Nature 368 (6466), 32-38 (1994)
94150718
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                                                                                                                                                                                                                                                                                                                                                                            Submitted by:
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/gene="C25E6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement (6056
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                                                                                                                                                                                                                                                                               3 (bases 1 to 43803)
Waterston, R.
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16243. ,208
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/ CEARSTACTOR TO STATE TO STAT
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24185. 24653,24703. 24875,24923. 25050,25114. 25196,
25344. 25495,25544. 26161,26225. 26956,27003. 27136,
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IVDNACALLDHQPNAVVPLMPTVFNYEILQLLTRCFRVDQLERPTFERLVKPFQD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="coded for by C. elegans cDNA yk28e9.3; coded for by C. elegans cDNA yk28e9.5; coded for by C. elegans cDNA yk28h9.3; coded for elegans cDNA yk28h9.5; coded for elegans cDNA yk48h9.5; coded for by C. elegans cDNA yk40e4.5; coded for by C. elegans cDNA yk5h3.5; weakly similar to dihydroorotate dehydrogenase
                                              IFGGLKCAHKSTKEEDCVHGTRALGDEIACLLQCGRHPRIVELFGVDESYNLLLEHVE
YGCIRNFWMASEAPLDTEFLVRICKDIYSAMAYLESIRIVHGHFTPNNILMDGEFHAK
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SSVFRLLEALKPVVYFYFQSQKLVDQFNFFNFQRPASKENRSEWEERLTEEGSMSHES
SEKAHKAIENVEDYCQTLTRHGNEELRTNLERVITTFKSNLMHSLLDIHDLYEQTLLS
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VNKHNMEEDVKNNLFIEAGGFQNNLYGTSIQSVRDVANQGRHCILDVSGNAIRRLQSN
PEGREEHTYSQPVSPENSSNGSYKSVRKIQALKKYPSSALLIGKAIGEGKFTMIKECI
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FGKYRDEREKLEAIKLSESNLLDTENYHFASRPDTQVSRVPTVEDVIGKALPRIGPYV
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SVCPIPECLEMVPRTGPWKAPKRGVKPSVEPGTPKVVKVDQRGRVILDTTGGMQ"
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36229. .36389,56443. .35794,56811. .37157,3716. .37684,
37743. .38266,38350. .38632,38680. .38801,38857. .38870,
38931. .38949,39228. .39253,39483. .39725)
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/db_xref="G1:1049458"
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/db_xref="GI:1049459"
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/gene="C25F6.3"
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/gene="C25F6.2"
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Query Match
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/db_xref="G1:1049460"
/db_xref="G1:1049460"
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/db_xref="G1:1064960"
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/db_xref="G1:1064960"
/d
ANIQPISIFIKPSSAQQILELDSQLATNRQDDRAMSGEEAQAQYSRCHRIEQTFGDLF
TQEISNTPIWVPQTLLLELRNLSFLLPSPSSPNSIHFLLEIVTVCDILNASFVSTNRK
SLSYSRLSTDEKLRLISIFWDFYYSESILFSSIGSKLFFFNYF"
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*** SEQUENCING IN PROGRESS ***, in ordered
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For further information on this sequence e-mail to fly@celera.com. * NOTE: This is a 'working draft' sequence. * This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 25784 TTGGACAAGGACTTGGTCACAATGTCTCCACGTATTGTCCGAGGATCTACCAGTGGA 25843
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          by the finished sequence as soon as it is available and the accession number will be preserved.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              join(41327. .41484,42079. .42208,42260. .42523)
/gene="C25F6.1"
/note="coded for by C. elegans cDNA CEESH77F"
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Pred. No. 0.00021;
0; Mismatches 64; Indels 0;
                                                                                                                                   /note="Met; codon recognized: ATG" 40305. .40377
                                                                                                                                                                                   "Met; codon recognized: ATG"
.40668
                                                                                                                                                                                                                                                                             /note="Met; codon recognized: ATG" 41327. .42523
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8218 c 7586 g 14438 t
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5227 c 5359 g
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/gene="C25F6.1"
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AC014157.1 GI:6437178
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Matches 109; Conservative
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fruit fly.
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SOURCE
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ILIN LILY.

INTERTYOLS MELAZOSA AITHOPODA; Tracheata; Hexapoda; Insecta;

Enkaryota; Metazos, Aithopoda; Tracheata; Hexapoda; Insecta;

Enkaryota; Metazos, Arthopoda; Tracheata; Hexapoda; Insecta;

Enkaryota; Metazos, Endopterygota; Diptera; Brachycera;

Mascamorpha; Ephydroidea: Drosophilidae; Drosophila.

I. (bases 1 to 30;09; Mortman, Jr. Yandell, M.D. Zahnago, V. A. Galer, R.F.,

Amanatidea; P.G., Scherer, S.E., Lip, W., Hoskins, R.M., Galer, R.F.,

Randon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D.,

Manklos, G.L., Abril, J.F., Agbayani, A., M.H., M. Hason, C.R., Gabor

Miklos, G.L., Abril, J.F., Agbayani, A., M.H., Hason, C.R., Gabor

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Shelber, Wang, A., W., W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AE003446 303092 bp DNA INV 04-OCT-2000
Drosophila melanogaster genomic scaffold 142000013386054 section 30
                                                                          0;
                                                                                                                                                                                   Db 14044 AGGATCTGGTCACGAATGTCTCGCCGCGCATCGTCAGGGGCACCACGTCGGGCTACAAGT 14103
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                                                                                                                                                                                                                                                                                     327 ATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCATCAGTGAGAAAACGGCTGCAT 386
   Length 24429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 14164 ACTGGCTGAAATCGATTGGAGAACTGAAGCGTGACTTCCCCGGAGAA 14209
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                                                                                                                                                                                                                                                                                                                                                                                                                                   387 ATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCCCAGACAA 432
   DB 63;
                                     Pred. No. 0.00027
                                                                       0; Mismatches
8.1%; Score 70;
63.9%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 35, complete sequence. AE003446 AE002566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AE003446.2 GI:10728536
                                                                   Matches 106; Conservative
                                     Similarity
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AKGFLGRIKRYSVLGNKLGRRNLGSMNLNPNNVVDNSVSPTKLHTGSVNMTGSHSDD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FETPKHEVEEKLLTANQDVKRPITPITIAIDPPIRRPRIARQQRQSVQNLHRSELK
VYLHKSNSVALDMNVTAPAKLGLDLNLPELPELYGASELSLAASDNKENLPAVKPSAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NQTLINFÜHNKEKLRKGWHGMKHWLGEEGSKIKEAVRQQTPLKRLAQSRSNLNQSTAD
ASRQSMSPERTQRDVTESCEDVTERTEMESSMSHRNSEEDLSPHAKRFKDEGQNGFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HTTLAMNRERRKHALIKLLQLVKTDLERERRSRDGLRCLSQSLNHQEHQNITDKLYHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRRYVKQGGDFSKELIFVLQERADSELIYSKSLSKLANKLNKAGREIPGSVADAWRGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATEMESRSDIHRQLAASLTDELVKPLKIVVEGHHKARKAVESNVDKAARVLGEWRASE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNKRKKAEEAVKRADVEYYTLCVRSERARVDWEMAVLRGSAQLQSSEQQRLGNMHNFA
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2 (bases 1 to 303092)
Adams, M.D., Celniker, S.E., Gibbs, R.A., Rubin, G.M. and Venter, C.J. Direct Submission
Submitsation
Submitsation
Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7290992.
Location/Qualifiers
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Van Gelder, R.N., Bae, H., Palazzolo, M.J. and Krasnow, M.A.
Direct Submission
Submitted (29-JUL-1996) Ophthalmology and Visual Sciences,
Washington University School of Medicine, 660 S. Euclid Avenue, Box
8096, St. Louis, MO 63110, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Van Gelder R.N., Bae, H., Palazzolo, M.J. and Krasnow, M.A. Extent and character of circadian gene expression in Drosophila melanogaster: identification of twenty oscillating mRNAs in the fly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GLPLDTPAALPLFYTDIDAVDISVEMCGIRFENPFGLASAPPTTSTAMIRRAFEGGWG
FVVTKTFGLDKDLVTNVSPRIVRGTTSGYKYGPQQGCFLNIELISEKRAEYWLKSIGE
LKRDFPEKIVIASIMCSFNEEDWTELAIKAEQSGADALELNLSCPHGMGERGMGLACG
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KADSTAWPAIGKEQRTTYGGVSGNATRPMALKAISDIANRVPGFPILGIGGIDSGEVA
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SIRRQARCPFDRRGKATLGFFGPYQRQRDIKMAELRSQKGALSWDAEQVKATPPASNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MEFCRTEQNENDEWVEDEEQTQRLKANFVISAFGSGLEDQDVKA
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EFDKDTHIPHVNDDCTGCTLCVSVCPIIDCITMVPKKIPHVIKRGVEEKIFYTHALSQ
                                                                                                                                                                     Db 165897 AGGATCTGGTCAGGCGCATCGTCGCGCATCGTCAGGGCCACCACGTCGGGCTACAAGT 165838
                                                                                                                                                                                                                                                                        Db 165837 ATGGACCCCAGCAGGCTGTTTCCTGAACATCGAACTAATCTCGGAGAAGCGGCCGAGT 165778
                                                                                                                                           267 AGGACATTGTGACAAATGTTTCCCCCATAATCATCGGGGGAACCACCTCTGGCCCCATGT 326
                                                                                                                                                                                                                                            327 ATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCATCAGTGAGAAAACGGCTGCAT 386
                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Epigroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="similar to dihydropyrimidine dehydrogenase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DMU65491 2348 bp mRNA INV 26-SEP-1
Drosophila melanogaster Dreg-3 protein mRNA, complete cds.
U65491
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                                                Length 303092
                                                                                                                                                                                                                                                                                                                                                                    Db 165777 ACTGGCTGAAATCGATTGGAGAACTGAAGCGTGACTTCCCCGGAGAA 165732
                                           8.1%; Score 70; DB 4; Length 303 ilarity .63.9%; Pred. No. 0.00027; Conservative 0; Mismatches 60; Indels
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/codon_start=1
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/protein_id="AAC47288.1"
/db_xref="GI:1561730"
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/note= "Encodes amino acids 581-635 of the DPD protein"
                                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus
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AAT14078
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AAD02175
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AAT91323
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 Fernandez-Salguero P,
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P-PSDB; AAW30092.
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Human dihydropyrim
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**SIDSB/gcgdata/geneseq_foneseq_NA1981.DAT:*

**SIDSB/gcgdata/geneseq_foneseq_NA1991.DAT:*

**SIDSB/gcgdata/geneseq_foneseq_foneseq_NA1991.DAT:*

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**SIDSB/gcgdata/geneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_foneseq_fo
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Compugen Ltd.
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               GenCore version
Copyright (c) 1993 - 2000
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Listing first 45 summaries
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Score

Result Š. 171.2 169.6 169.6 169.6 153.4 153.4 151.4 151.4

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                                                                                              A novel method has been developed for detecting the splicing defect in the dihydropyrimidine dehydrogenase (DPD) gene. The method comprises determining whether genomic DNA containing the DPD gene has a wild-type intron-exon boundary for an exon that encodes amino acids (aa) 581-635 of the corresponding DPD protein. The present sequence represents a DPD genomic fragment which encodes the amino acids 581-635. The method is used specifically to determine sensitivity of subjects to the anticancer agent 5-fluorouracil, which is dangerously toxic to those with DPD defects. It can also be used to diagnose DPD-deficiency
                                                                                                                                                                                                                                                                                                                                                                                                                               AATTTATCTGGAGCTAACAATACTTTATTTTACCTTTTTATTTGCAAGTAGTTTATGTT 120
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          tecting a splicing defect in the di:hydro:pyrimidine dehydrogenase one - used to identify subjects sensitive to 5-fluorouracil, toxic individuals with DPD defects
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                                                                                                                                                                                                                                                        Sequence 861 BP; 300 A; 140 C; 161 G; 260 T; 0 other;
                                                                                                                                                                                                                                                                                                 99.6%; Score 857.8; DB 18; 99.8%; Pred. No. 7.1e-183; ive 0; Mismatches 2;
                                                                   Disclosure; Fig 1; 38pp; English
                                                                                                                                                                                                                             disorders such as uraciluria.
                                                                                                                                                                                                                                                                                                                               Conservative
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Matches 859; Conser
                Detecting
                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   780
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                                                                       721 CACTGTATGTGGCTGGTATTTATGAAGGTGATGACCCAGGAAGAAATTGTAAAACTATAAA
             CCACTCCAAATATAAACCCGAGGCAGAAGCAGCATATCTCCCTATGAAGCCTGTATTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oclonal antibody specific for dihydropyrimidine dehydrogenase assessing patient response to 5-fluorouracil antitumor agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This invention describes a monoclonal antibody (MAb) specific for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 20; Length 3951;
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                                                                                                                                                                                                                                                                                                                                   DPD; dihydropyrimidine-dehydrogenase; monoclonal antibody; immunoassay reagent; cancer patient; treatment; antitumour 5-fluorouracil; affinity purification; toxicity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and suitable for routine screening.
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93.2%; Pred. No. 2.4e-29;
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P-PSDB; AAW93361.
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Matches 179; Conser
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244 CTCAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCCATAATCATCCG 303
The DPD gene, DPYD, is located at chromosome 1p22. The cDNA can be inserted into a vector and used for prodn. of DPD (AAR91420) in transformed host cells, or used as a selectable marker that functions in prokaryotic and eukaryotic cells. It can also be utilised as a probe to detect DPD deficiency in an individual, i.e. to identify risk of toxic reaction to 4-fluorouracil.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovine; liver; human; dihydropyrimidine dehydrogenase; DPD; pyrimidine catabolism; 5,6-dihydropyrimidine; pyrimidine analogue; fluoropyrimidine; anticancer drug; 5-fluorouracil; FUra; cancer;
                                                                                                                                                                                                                                                                                    304 GGGAACCACCTCTGGCCCCATGTATGCCCCTGGACAAGCTCCTTTCTGAATATTGAGCT
                                                                                                                                                                                                                                                                                                                                                 CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTT
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                                                                                                                                                                                          14; Indels
                                                                                                           Sequence 3957 BP; 1156 A; 787 C; 897 G; 1117 T; 0 other;
                                                                                                                                                        DB 17;
                                                                                                                                                        Score 169.6; DB 17
Pred. No. 5.4e-29;
0; Mismatches 14,
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/product= DPD
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92.7%;
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                                                                                                                                                                                         178; Conservative
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P-PSDB; AAR86001.
                                                                                                                                                       Query Match
Best Local Similarity
Matches 178; Conserv
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                                                                                                                                                                                                                                                                                                                              Dihydropyrimidine dehydrogenase; DPD; DPVD gene; probe; deficiency; 5-fluorouracil; cytostatic; cancer; selectable marker; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pig and human di:hydro:pyrimidine dehydrogenase (DPD) genes and probes - useful for detection of DPD deficiencies and identification of humans at risk of toxic reaction to 5-fluoro:uracil anti-cancer treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human dihydropyrmidine dehydrogenase (DPD) cDNA (AAT14077) was isolated as 3 overlapping fragments obtd. from human liver cDNA libraries screened using pig DPD cDNA (see also AAT14077).
                                                                                                                                                                                                                                                                                                 Human dihydropyrimidine dehydrogenase cDNA
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/note= "primer RTF1"
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88..3165
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This sequence represents the DNA sequence encoding human dihydropyrimidine dehydrogenase (DPD). DPD catalyses the initial and rate limiting step in pyrimidines. DPD catalyses the initial pyrimidines to 5.6-dihydropyrimidines. DPD is a complex enzyme consisting of two identical subunits, containing FMN. FAD and ironsulphur centers, and utilising NADPH as a cofactor. DPD has also been shown to catalyse the reduction of various pyrimidine analogues including the fluoropyrimidine anticancer drug 5-fluorouracil (FUra). Up to 85% of administered FUra may be catabolised by DPD, and it therefore governs the effectiveness of FUra as an anticancer drug. DPD genes or fragments of them may be used in the detection of DPD in a sample, esp. isolated from a cancer patient. According to the amount of DPD detected, a therapeutically effective amount of FUra may be determined and administered. DPD deficiency, leading to lifethreatening toxicity on exposure to FUra, in a human caused by a frameshift mutation may be determined by means of a molecular biological assets.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             364 CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTT
                                                                                                                                                                                                                                                                                        Length 4368;
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                                                                                                                                                                                                                                                  Sequence 4368 BP; 1325 A; 829 C; 932 G; 1282 T; 0 other;
                                                                                                                                                                                                                                                                                      DB 16;
                                                                                                                                                                                                                                                                                      19.7%; Score 169.6; DB 16
92.7%; Pred. No. 5.5e-29;
iive 0; Mismatches 14;
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/product= Human lymphocyte DPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human dihydropyrimidine dehydrogenase cDNA.
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1260..1288
/*tag= d
3117..3139
/*tag= e
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                                                                                                                                                                                                                                                                                                  Best Local Similarity 92.7
Matches 178; Conservative
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/*tag= 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             424 CCCAGACAACGT 435
                                                                                                                                                                                                                        DPD-coding region.
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This sequence represents the CDNA sequence encoding human dihydroperase (DPD). This sequence was amplified using the primer sequences given in AAT031447. DPD catalyses the initial catalyses the initial catalyses the initial primedione catabolism, the reduction of pyrimidines to 5,6-dihydropyrimidines. DPD is a complex enzyme consisting of two identical subunits, containing FWN. FND and isoben subpur centers, and utilising NADPH as a cofactor. DPD has also been shown to catalyse the reduction of various pyrimidine analogues including the fluoropyrimidine anticancer drug 5-fluoropyrimidine anticancer drug. Up to 85% of administered FUra may be catabolised by DPD, and it therefore governs the effectiveness of FUra as an anticancer drug. DPD genes or fragments of them may be used in the detection of DPD in a sample, esp. isolated from a cancer patient. According to the amount of DPD detected, a therapeutically effective amount of FUra may be determined and administered. DPD deficiency, leading to lifethreatening toxicity on exposure to FUra, in a human caused by a frameshift mutation may be determined by means of a molecular biological assay to detect the deletion of an A residue at codon 318 within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1824 gggaaccacctctggccccatgtatggccctggacaaagctcctttctgaatattgagct 1883
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Best Local Similarity 92.7%; Pred. No. 5.5e-29,
Matches 178; Conservative 0; Mismatches 14
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This sequence represents the cDNA sequence encoding bovine liver dihydropyrimidine dehydrogenase (DPD). This sequence was isolated using the primers given in AAT03134-41 and AAT14638. DPD catalyses the initial and rate limiting step in pyrimidine catabolism, the reduction of pyrimidines to 5,6-dihydropyrimidines. DPD is a complex enzyme consisting of two identical subunits, containing FMN, FAD and iron-
1905 tcagtgaaaaaacggctgcatattggtgtcaaagtgtcactgaactaaaagccgactttc 1964
                                                                                                                                                                                                                                                                                                      Bovine, liver; human; dihydropyrimidine dehydrogenase; DPD; pyrimidine catabolism; 5,6-dihydropyrimidine; pyrimidine analogue; fluoropyrimidine; anticancer drug; 5-fluorouracil; FUra; cancer; frameshift mutation; ss.
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57..3144
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/note= "Primer A"
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/note= "Primer B"
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/note= "Primer
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/note= "Primer
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                                   426 CAGACAA 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents the DNA sequence encoding bovine liver dihydropyrimidine dehydrogenase (DPD). DPD catalyses the initial and rate limiting step in pyrimidines catabolism, the reduction of pyrimidines to 5.6-dihydropyrimidines. DPD is a complex enzyme consisting of two identical subunits, containing FMN, FAD and ironsulphur centers, and utilising NADPH as a coffector. DPD has also been shown to catalyse the reduction of various pyrimidine analogues. Up to 85% of administered FUR may be catabolised by DPD, and it therefore governs the effectiveness of FUR as an anticancer drug. DPD genes or fragments of them may be used in the detection of DPD in a sample, esp. isolated from a cancer patient. According to the amount of DPD detected, a therapeutically effective amount of FUR amp be determined and administered. DPD deficiency, leading to lifethremeshift mutation may be determined by means of a molecular biological assay to detect the deletion of an A residue at codon 318 within the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                  Bovine; liver; human; dihydropyrimidine dehydrogenase; DPD; pyrimidine catabolism; 5,6-dihydropyrimidine; pyrimidine analogue; fluoropyrimidine; anticancer drug; 5-fluorouracil; FUra; cancer;
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88.8%; Pred. No. 2.3e-25;
Live 0; Mismatches 21; Indels 0;
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                                                Bovine dihydropyrimidine dehydrogenase gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 115-32; 207pp; English.
                                                                                                                                                                                                               Location/Qualifiers
68..3145
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                                                                                                                                                                                                                                                                      /product= DPD
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         shown to catalyse the reduction of various pyrimidine analogues including the fluoropyrimidine anticancer drug 5-fluorouracil (FUra). Up to 85% of administered FUra may be catabolised by DPD, and it therefore governs the effectiveness of FUra as an anticancer drug. DPD genes or fragments of them may be used in the detection of DPD in a sample, esp. isolated from a cancer patient. According to the amount of PDD detected, a therapeutically effective amount of FUra may be determined and administered. DPD deficiency, leading to life-threatening toxicity on exposure to FUra, in a human caused by a frameshift mutation may be determined by means of a molecular biological ssay to detect the deletion of an A residue at codon 318 within the
 DPD has also been
                                                                                                                                                                                                                                                                                            1784 ccaaaactttctctttgataaggatatagtgacaaatgtttcacccagaatcatccggg 1843
                                                                                                                                                                                                                                                                                                                                             1844 ggaccacctctggccccatgtatggccctggacaaagctctttcctgaatattgagctca 1903
                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                                                                                                                                   246 CAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCCATAATCATCGGG 305
                                                                                                                                                                                                                                                                                                                                                                      TCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCC 425
                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                   Length
                                                                                                                                                                                                       Score 153.4; DB 1b; Level Pred. No. 2.38-25;
                                                                                                                                                                          Sequence 4430 BP; 1333 A; 871 C; 955 G; 1271 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETM; mismatch; genotyping;
 sulphur centers, and utilising NADPH as a cofactor.
                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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88.8%;
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                                                                                 Query Match 17.8
Best Local Similarity 88.8
Matches 166; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide D1835
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                                                                                                                                                     DPD-coding region.
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present invention relates to a composition comprising two nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 ATTTAATGTATATAAAATTCCTCTGCAAATATGTGAGGGGGGGCCTCATAAAATATTG 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309 CCACCTCTGGCCCCATGTATGGCCCTGGACAAGCTCCTTTCTGAATATTGAGCTCATCA 368
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 CCAGTIGCTITGCTGATGCATAGAAAGATAAAAAAGAAAGAAAAGCTCAAGAACTCATAA 608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTGGCTGGTATTTATGAAGGTGATGACCCAGGAAGAATTGTAAACTATAAACCACTCCA 788
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                                                                                                                                                                                                                                                                                                                                                                                                                                             9 AAGATAAATATTTTGTTTTTCGCTGTTCTAAACCTAGGGTTACAAGAAGTAATTTATC 68
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                                                                                                                                                                                                                                                                                                                   Length 936,
                                                                                                                                                                                                                                                                                                                   17.6%; Score 151.4; DB 22; 1.0%; Pred. No. 4.6e-25;
                                                                                                                                                                                                                   Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other
                                                                                                                                                                                                                                                                                                                                             ilarity 1.0%; Pred. No. 4.6e-25;
Conservative 511; Mismatches 272;
                                                                                                                                                       monitoring gene expression.
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                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 8; Conserv
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group, useful as labels in allowing repeat analyses on
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     369 GTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCCCAG 428
                                                                         429 ACAACGTAAGTGTGATAAAAATCTAAAACAAGAGAATTGGCATAAGTTGGTGAATGTTTA 488
                                                                                                                                                                                                                                                                                                                                                            669 TACATAAGCAGAAGGAAGAGAAATGAAATACTCATTTTATTGAGTTGGCCCCCACTGTAT 728
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                                        489 TTTAAACATCCAATTCATAGGCTTATAAATATTAATGTGTATATTTATCAACGAATCTG
                                                                                                                                                                                                                    609 AAACCCACACAATGTGAAGCTCTGTTATAAATGGGTGCCATGTAAGATGGAAGAAGTATC
                                                                                                                                                                                                                                                                                                                         Electron-transfer group; ETM; mismatch; genotyping;
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                            Electron-transfer group; ETM; mismatch; genotyping;
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                  AAF58254 standard; DNA; 936 BP.
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1.0%; F
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17-MAR-2000; 2000US-0190259.
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  single-nucleotide polymorphisms, e.g. for genotyping,
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                                                                      DB 22;
                                                                                 Similarity 1.0%; Pred. No. 4.6e-25; 8; Conservative 511; Mismatches 272;
                                   other
                              Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776
                                                                       Score 151.4;
                                                                      17.68;
             monitoring gene expression.
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AAF58259 standard; DNA; 936

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                                                      ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 151.4; DB 22;
Pred. No. 4.6e-25;
1; Mismatches 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 936 BP; 6 A; 138 C; 8 G; 8 T; 776 other;
                                                                                                                                                                                                                                                                                                                               electron-transfer
J. for genotyping,
                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Page 128; 159pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.6%; Sco
Best Local Similarity 1.0%; Pred
Matches 8; Conservative 511;
                                                                                                                                                                                                                                                (CLIN-) CLINICAL MICRO SENSORS
                                                                                                                                                                              2000WO-US20476
                                                                                                                                                                                                         26-JUL-1999; 99US-0145695
17-MAR-2000; 2000US-0190259
                                                                                                                                                                                                                                                                                                                                            e.g.
24-APR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                               containing
assays, e.g
                                                      Electron-transfer group;
                            Oligonucleotide D2004
                                                                  gene expression; ss
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                                                                                                                                                                                                                                                                                                                                                          a single surface
                                                                                                                         WO200107665-A2.
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hybridization
                                                                                                                                                                              26-JUL-2000;
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                                                                                              Synthetic.
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661
                                                                                                                                                                                               GTGGCTGGTATTTATGAAGGTGATGACCCAGGAAGAAATTGTAAACTATAAACCACTCCA 788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention relates to a composition comprising two nucleic
                                                                                                                                                                                                                   acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping,
                                                                                                                            AAACCCACACAATGTGAAGCTCTGTTATAAATGGGTGCCATGTAAGATGGAAGAAGTATC
                                                                                                                                                      TACATAAGCAGAAGGAAGAGAAATGAAATACTCATTTTATTGAGTTGGCCCCCCCTGTAT
                              489 TITAAACAICCAATICATAGGCITATAAATAITAAAIGTGTATAITITAICAACGAAICIG
                                                Electron-transfer group; ETM; mismatch; genotyping; gene expression; ss.
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17-MAR-2000; 2000US-0190259.
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                                                                                                                                                    69 TGGAGCTAACAATACTTTATTTTACCTTTTTATTTGCAAGTAGTTTATGTTCAATTCTA 128
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                22;
                                                272;
                1.4; DB;
4.6e-25;
                                  ilarity 1.0%; Pred. No. 4.6e-
Conservative 511; Mismatches
                Score 151.4;
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Query Match
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WO9608568-A2
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1.0%; Pred. No. 4.6e-25;
Live 511; Mismatches 272;
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17-MAR-2000; 2000US-0190259
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Matches 8; Conserv
  gene expression;
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Dihydropyrimidine dehydrogenase; DPD; DPYD gene; probe; deficiency; 5-fluorouracil; cytostatic; cancer; selectable marker; ss.
                                                          AAACCCACACAATGTGAAGCTCTGTTATAAATGGGTGCCATGTAAGATGGAAGAAGTATC
                                                                                                                                                                                                                                                             TACATAAGCAGAAGGAAGAGAAATGAAATACTCATTTTATTGAGTTGGCCCCCCCTGTAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGGCTGGTATTTATGAAGGTGATGACCCAGGAAGAAATTGTAAAACTATAAACCCACTCCA
                                                                                                                            isolated from a pig liver cond library by screening with a polyclonal antibody raised against pig DPD, and rescreening using an isolated partial CDNA. The DPD cDNA can be inserted into a vector and used for prodn. of active DPD (AAR91421) in transformed host cells, e.g. Escherichia coll, or used as a selectable marker functional in prokaryotic and eukaryotic cells. It can also be utilised as a probe to detect DPD deficiency in an individual, i.e. to identify risk of toxic reaction to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pig and human di:hydro:pyrimidine dehydrogenase (DPD) genes and probes - useful for detection of DPD deficiencies and identification of humans at risk of toxic reaction to 5-fluoro:uracil anti-cancer treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pig dihydropyrmidine dehydrogenase (DPD) cDNA (AAT14078) was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dihydropyrimidine dehydrogenase cDNA.
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88..3165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAT14078 standard; cDNA; 4447 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gonzalez
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               789 AATATAAACCC 799
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on
                                                                                                                                                     1805 ccaaaactttctctcttgataaggacatagtgacaaatgtctcacccagaatcgtccggg 1864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.
                                                                                              246 CAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCCATAATCATCCGGG 305
                                                                          0; Gaps
                                                                                                                                        GAACCACCTCTGGCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCA
                                                                                                                                                                                    TCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCC
                                                                                                          Score 150.2; DB 17; Length 4447;
Pred. No. 1.2e-24;
); Mismatches 23; Indels 0;
                      0 other;
                                                                                                                                                                                                                                                                                                                                                                                           Electron-transfer group; ETM; mismatch; genotyping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
                     Sequence 4447 BP; 1285 A; 928 C; 1000 G; 1234 T;
                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 6; Page 127; 159pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CLIN-) CLINICAL MICRO SENSORS INC
                                                                                                                                                                                                                                                                                                      AAF58252 standard; DNA; 936 BP.
                                                     17.48;
87.78;
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                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                  Query Match 17.4
Best Local Similarity 87.7
Matches 164; Conservative
                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide D1835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-159728/16.
                                                                                                                                                                                                                                                                                                                                                                                                        gene expression; ss
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1985 cagacaa 1991
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 4-fluorouracil.
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17-MAR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
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                                                                                                                                                                                                                                 132 TAATGTATATTAAAAATTCCTCTGCAAATATGTGAGGAGGGACCTCATAAAATATTGTCA 191
                                                                                                                                                                                                                                                                                                                                                                                                 CITTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCATAATCATCGGGGGAACCA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      672 ATAAGCAGAAGGAAGAGAAATGAAATACTCATTTTATTGAGTTGGCCCCCACTGTATGTG 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         732 GCTGGTATTTATGAAGGTGATGACCCAGGAAGAAATTGTAAACTATAAACCACTCCAAAT 791
                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 312 CCTCTGGCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCATCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAATATTTTTTTTTTTCCTGTTCTAAACCTAGGGTTACAAGAAGTAATTTATCTGG
                                                                                                                                            72 AGCTAACAAATACTTTATTTTACCTTTTTTTTTTGCAAGTAGTTTATGTTCAATTCTAATT
                                                                                                                                                                                        192 TATGGAAATGAGCAGATAATAAAGATTATAGCTTTTCTTTGTCAAAAGGAGACTCAATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      552 GTTGCTTTGCTGATGCATAGAAGATAAAAAGAAAGAAAAGCTCAAGAACTCATAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGTAAGTGTGATAAAAATCTAAAACAAGAGAATTGGCATAAGTTGGTGAATGTTTATTT
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                         .;
0
                         Indels
3.6e-24;
tches 271;
    Pred. No. 3.6e-;
0; Mismatches
ilarity 0.5%; Pre Conservative 510;
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Search completed: November 20, 2001, 15:59:11 Job time: 5375 sec

Query Match

17.1%; Score 147.4; DB 22; Length 936;

em\_esthum12:\*
em\_esthum13:\*
em\_esthum14:\*

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991:
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                                                                                                                                                                                                                                                                                            November 20, 2001, 14:25:51; Search time 1355.35 Seconds (without alignments) 6005.022 Million cell updates/sec
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861
1 TGTTAATGAAGATAAATATT......AGTGGGAAATAATTATTAA 861
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10228115 seqs, 4726426750 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                   OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 2000000000
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em_esthum1:*
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em_esthum9:*
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gb_est39:*
gb_est40:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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em\_estpl6:\*
em\_estpl6:\*
em\_estpl6:\*
em\_estpl7:\*
em\_estpl8:\*
em\_estpl9:\*

em\_estov2:\*
em\_estpl1:\*
em\_estpl2:\*
em\_estpl3:\*

em\_estro19:\*
em\_estro20:\*
gb\_est26:\*
gb\_est28:\*
gb\_est28:\*
gb\_est28:\*
gb\_est31:\*
gb\_est41:\*
gb\_est41:\*
gb\_est41:\*
gb\_est47:\*

em\_estrol1:\*
em\_estrol2:\*
em\_estrol3:\*
em\_estrol6:\*
em\_estrol6:\*
em\_estrol6:\*
em\_estrol8:\*

em\_estro8:\* em\_estro9:\* em\_estro10:\*

em\_estro4:\*
em\_estro5:\*
em\_estro6:\*
em\_estro7:\*

em\_estrol:\* em\_estro2:\* em\_estro3:\* gb\_est110:\*
gb\_est111:\*
gb\_htc:\*
em\_gss\_fun:\*
em\_gss\_hum1:\*

em\_gss\_hum3:\* em\_gss\_hum4:\* em\_gss\_hum5:\*

em\_gss\_hum6:\* em\_gss\_hum7:\* em\_gss\_hum8:\*

em\_gss\_hum9:\* em\_gss\_inv1:\* em\_gss\_inv2:\* em\_gss\_other:\*

em\_gss\_inv3:

em\_gss\_pln1:\* em\_gss\_pln2:\*

em\_gss\_pro:

em\_gss\_rod1:\* em\_gss\_rod2:\* em\_gss\_rod3:\*

em\_gss\_rod4:\*
em\_gss\_rod5:\*
em\_gss\_vrt1:\*
em\_gss\_vrt2:\*
em\_gss\_vrt3:\*
gb\_gss1:\*

gb\_gss4:\* gb\_gss5:\*

gssb\_dg

gb\_gss3:\*

\*:8886\_dp

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9b-9ss10. 9b-9ss11... 9b-9ss13... 9b-9ss15... 9b-9ss187... 9b-9ss19... 9b-9ss19...

9b\_9ss20... 9b\_9ss21... 9b\_9ss23... 9b\_9ss24... 9b\_9ss25... 9b\_9ss26...

gb\_gss27:\* gb\_gss28:\* gb\_gss29:\*

gb\_gss30:\*

255: em\_gss\_rodb:\*
256: gb\_gss35:\*
257: gb\_gss36:\*
258: gb\_gss37:\*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em\_gss\_inv4:\*

gb\_gss31:\* gb\_gss32:\* gb\_gss33:\*

Result Š

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July 1938

/ Organism="Homo sapiens"
/ Organism="Homo sapiens"
/ Organism="Image: 182302"
/ Clone="Image: 182302"
/ Clone="Image: 19mphoma, cell line"
/ Lab_host="DH10B (phage-resistant)"
/ Absue_type="lymphoma, cell line"
/ Lab_host="DH10B (phage-resistant)"
/ Anote="Organ: lymph; Vector: pcWV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NH_MCC Library."
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
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Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSUZEE1 853 bp DNA GSS 13-MAY-2000
Tetraodon nigroviridis genome survey sequence T7 end of clone 262A08 of library G from Tetraodon nigroviridis, genomic survey
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis Staudt, M.D., Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
http://image.llnl.gov
High quality sequence stop: 714.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                244 CTCAATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCCATAATCATCCG
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Pred. No. 7.9e-29;
0; Mismatches 14
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92.7%;
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Best Local Similarity 92.7
Matches 178; Conservative
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 938)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                         Description
                                                                                                                                                               AU086287 BF653737
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AZ527678
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cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by:
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1 (bases 1 to 621)

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R.
                                                                                                                                                     a large
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fd60d03.yl Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to
SW:DPYD_HUWAN Q12882 DIHYDROPYRIMIDINE DEHYDROGENASE [NADP+]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ·,
               Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                 Genoscope.

Direct Submission

Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases

This sequence is a single read and was generated as part of a larr

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         ID : COAG262BA04LP1~end : T7"
t 7 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 318 GCCCCATGTATGGCCCTGGACAAAGCTCCTTTCTGAATATTGAGCTCATCAGTGAGAAAA 377
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1800
Email: zbrafish@watson.wustl.edu
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Pred. No. 3.8e-11;
1; Mismatches 57; Indels
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/db_xref="taxon:99883"
/clone="262A08"
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189 c 136 g 269
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Unpublished (1998)
Saurin, W. and Weissenbach, J.
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AW018806
AW018806.1 GI:5872336
                                                                                                                                                                                                                                                                                                                           /clone_lib="G"
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double-stranded chank was ligated continuining to be depended to digested with Not I and cloned into the Not I and Sal I sites of the pSPORTI vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik, Berlin). CDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from cebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single CDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality.
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0
Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@esesgen.com) and Ressourcen@entrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster genome survey sequence TET3 end of BAC # EACR03G12 of RPCI-98 library from Drosophila melanogaster (fruit lly), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="26 somite embryos, adult livers, shield
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1207)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 86.2; DB 110; Length 621;
Pred. No. 1e-09;
0; Mismatches 48; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                 /organism="Danio rerio"
/db_xref="taxon:7955"
/clone_lib="Zebrafish WashU MPIMG EST"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAGCGTGGCTGAACTCAAAGCCGACTTCCCCAAAAATATTA 163
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/lab_host="XL1-blue MRF"
                                                                                                                                                                                           www.rzpd.de)
Seq primer: T3 ET from Amersham
High quality sequence stop: 491.
Location/Qualifiers
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Best Local Similarity 70.6%;
Matches 115; Conservative (
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Direct Submission

L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
- Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or fillters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                        /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit AL063921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 CATCAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTT 423
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1 (bases 1 to 1101)
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/db_xref="taxon:7227"
                                                                                                                                                                             /db_xref="taxon:10090"
/clone="IMAGE:3490423"
/clone=lib="NCI_CGAP_Mam5"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
/lab_host="DH10B"
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           Plate: LLAM8532 row: p column: 08
                                                                                               1. .562
/organism="Mus musculus"
                                      High quality sequence stop: 562.
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                                                                                                                                                        /strain="C57/B6"
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                                                                                                              Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC ibrary was prepared by Kazutcyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2: cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                             Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 562)
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 AGGACATTGTGACAAATGTTTCCCCCATAATCATCCGGGGAACCACCTCTGGCCCCATGT 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399 AGGATCTGGTCACGAATGTCTCGCCGCGATCGTCAGGGGCACCACGTCGGGCTACAAGT 458
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Pred. No. 5.3e-06;
0; Mismatches 60; Indels 0
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/db_xxef="texon:7227"
/db_xref="texon:7227"
/clone_lib="RPCI-98"
/clone="BACR03G12"
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Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 500)
Watanabe,J., Sasaki,M., Suzuki,Y. and Sugano,S.
FULL.malaria: a database for a full-length enriched cDNA library from human malaria parasite, Plasmodium falciparum
Nucleic Acids Res. 29 (1), 70-71 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUG86287 500 bp mRNA EST 27-JAN-2001
AUG86287 Sugano Malaria CDNA library Plasmodium falciparum CDNA
Clone XPFn2249, mRNA sequence.
AUG86287
                                                                                                                                                                                 70 GGAGCTAACAAATACTTTATTTTACCTTTTTTTTTGCAAGTAGTTTATGTTCAATTCTAA 129
                                                                                                                                                                                                                       130 TTTAATGTATATTAAAAATTCCTCTGCAAATATGTGAGGGGGGCCCTCATAAAATATTGT 189
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                                                                                                                                  Gaps
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The University of Tokyo, Department of Parasitology
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
                                             503 others
                                                                                                                                  Indels
                                                                                                                                  232;
                                                                                                     DB 219;
                                                                                                    6.7%; Score 58; DB 21 ilarity 20.4%; Pred. No. 0.003; Conservative 216; Mismatches 2
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/clone_11b="RPCI-98"
/clone="BACR08K10"
/note="end : TET3"
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Contact: Junichi Watanabe
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CE 1 (bases 1 to 483)

RS Smith, T.P. L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,

RS Smith, T.P. L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,

Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid

W.W. and Keele, J.W.

Design and use of four pooled tissue normalized cDNA libraries for

EST discovery in cattle

Unpublished (2000)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4336

Fax: 402 762 4336

Fmail: smith@email.marc.usda.gov

Single pass sequencing. Bases called and alt_trimmed with phred

v0.980904.e. Vector identified by cross_match with the -minscore 18

PORR PRIMORS
Tel: 81-3-5449-5378
Fax: 81-3-5449-5410
Enail: jwatanab@anage.ims.u-tokyo.ac.jp
Suzuki,Y., Yoshitomo-Nakagawa,K., Maruyama,K., Suyama,A. and Sugano,S. Construction and characterization of a full length-enriched and a 5'-end-enriched cDNA library Gene 200 (1-2), 149-156 (1997).

Location/Qualifiers
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TCTGGAGCTAACAATACTTTATTTTACCTTTTTATTTTGCAAGTAGTTTATGTTCAATTC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 TAATTTAATGTATATTAAAAATTCCTCTGCAAATATGTGAGGAGGGACCTCATAAAATAT 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 322 AAATAAAATCCATATATATATATATATAAATAAAACATTTTATAAATATATATAAAAT 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                262 TATATTCTGACATATAATTTATTTTATTTTTAAAGAATTTNNTATAAGTTCAAAAT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 TGAAGATAAATATTTTTTTTTTTCGCTGTTCTAAACCTAGGGTTACAAGAAGTAATTTA 66
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277669 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
BF653737
                                                                                                                                                                                                                                                                                                                                                                                                                 6 others
                                                                                                                                                                                                                                                                                                             /clone_1xPFn2249"
/clone_1lb="Sugano Malaria cDNA library"
/dev_stage="erythrocytic stage"
25 c 24 g 231 t 6 other:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 55; DB 107;
Pred. No. 0.014;
0; Mismatches 140;
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. //organismin="3D7"
/strain="3D7"
/db_xref="taxon:5833"
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Best Local Similarity 49.3%;
Matches 136; Conservative
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Direct Submission Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage: BP 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr Determination of this BAC-end sequence was carried out as part of acilaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etded un Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CNSO020C 1101 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACNO1C19 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                                                                                                                                                                                                                            61 AATTTATCTGGAGCTAACAATACTTTATTTTACCTTTTTATTTGCAAGTAGTTTATGTT 120
                                                                                                                                                                                                                                                                                                                                                                                            121 CAATTCTAATTTAATGTATTAAAAATTCTCTCTGCAAATATGTGAGGAGGGACCTCATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 543 TITITITAMIAMAMWIWAAAWAAIWAWWWAAAAAIWWWWIWIITITITATIAWIAAWAIT 484
                                                                                                                                                   Gaps
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[ (bases 1 to 1101) Genoscope.
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                                                                                                Length 1101;
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     others
                                                                                                ; Score 52.6; DB 219; Length
; Pred. No. 0.051;
51; Mismatches 127; Indels
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/plasmid="pBeloBAC11"
  232
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/clone="BACN01C19"
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Matches 66; Conservative
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Web: www.genoscope.ons.fr.

Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCT-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's pl and EST libraries. A more detailed describtion of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                            /tissue_type="pooled"
/lab_host="Phel"pooled"
/lab_host="Phel"pooled"
/note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar marcophage, ovary, fetal semitendonosus muscle, and fetal longissimus muscle."
105 c 138 g 112 t
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Submitted (02-JUN-1999) Genoscope · Centre National de Sequencage
BP 191 91006 EVRY cedex · FRANCE (E-mail : seqref@genoscope.cns.fr
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Drosophila melanogaster genome survey sequence T7 end of BAC:
BARR29B23 of RPCI:98 library from.Drosophila melanogaster (fruit
fly), genomic survey sequence.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 53.4; DB 151; Length 483;
Pred. No. 0.032;
0; Mismatches 6; Indels 1;
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
                      Plate: 70 row: B column: 4 Seg primer: ATTTAGGTGACACTATAG.
BACKWARD: GTTTTCCCAGTCACGACG
                                                                       Location/Qualifiers
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Best Local Similarity 90.7%;
Matches 68; Conservative
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr
BP 191 91006 EVRY cedex - FRANCE (E-mail: seqrefégenoscope.cns.fr
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Drosophila melanogaster genome survey sequence T7 end of BAC
BACN1LL11 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
                                                                                                                                                                  GACTICCCAGACAACGIAAGIGIGAIAAAAAICIAAAAACAAGAGAAIIGGCAIAAGIIGG 478
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                                                                                          MAACTANTTTAAAAMMHMMAAAAAAWWAAAAAAAAAAAATTTTTYTTTWAWAHWTWTA
                 479 IGAATGTTTAATTTAAACATCCAATTCATAGGCTTATAAATATTAATGTGTATATTTATC
                                                                                                                                            247 AATATCTTTACTCTTTCATGAGGACATTGTGACAAATGTTTCCCCCATAATCATCCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             957 KKTATGTTTKTTTTWATGWATGTGKRATGWAGAAWGGTTTGTTGDAAAATGKRWAWATG
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1025)
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                                                                                                                                                                                                                     GAACTCATAAAAACCCACACAATGTGAAGCTCTGTTATAAAT 640
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/plasmid="pBeloBAC11"
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33.5%; Pred. No. 0.057
tive 83; Mismatches
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Plasmid Drosophila melanogaster
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/clone="BACN11L11"
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/strain="HM1:IMSS"
/db\_xref="taxon:5759"
/clone\_lib="Entamoeba histolytica Sheared DNA"
/clone\_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: PHOS1; Site\_l: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoba histolytica: a method for isolate identification. Exp. Parasitol. 77:480.). The DNA was mechanically sheared to give a tight size distribution (-2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)." the Entamoeba histolytica HM1:IMSS sheared AZ527678 912 bp DNA GSS 03-NOV-2000 ENTBN23TR Entamoeba histolytica Sheared DNA Entamoeba histolytica from Entamoeba histolytica 837 AARWAAAAAAAAAAAGWKAGARKGGAGAAAAATGKGGTGWRAAAAAAAAAAAAAAGKTG 778 367 CAGTGAGAAAACGGCTGCATATTGGTGTCAAAGTGTCACTGAACTAAAGGCTGACTTCCC 426 487 TATTTAAACATCCAATTCATAGGCTTATAAATATTAATGTGTATATTTATCAACGAATC 546 717 ARAWAWAAAATATAAATAWAYGAAKTGRAAAAAAAAAAAAAAAAATGTRAWAWATAWTTT 658 607 AAAAACCCACACAATGTGAAGCTCTGTTATAAATGGGTGCCATGTAAGATGGAAGAAGTA 666 427 AGACAACGTAAGTGTGATAAAAATCTAAAACAAGAGAATTGGCATAAGTTGGTGAATGTT 657 KKATTGTGAATWKGTTKGTKKAWAAAAAAWAAAAWAKWRWTAAWKKTARAAWDGTKKT USA 667 TCTACATAAGCAGAAGGAAGAAATGAAATACTCATTTTATTGAGTT MD 20850, /organism="Entamoeba histolytica" Entamoeba histolytica Entamoeba histolytica 1 (bases 1 to 912) Loftus, B., Van Aken, S. and Fraser, C. Determination of Clone end sequences HM1:IMSS sheared DNA library Unpublished (2000)
Contact: Brendan J Loftus
Contact: Brendan J Loftus
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tal: 301 838 0208
Fax: 301 838 0208 High quality sequence start: 20 High quality sequence stop: 734. Location/Qualifiers Email: bjloftus@tigr.org Clones are derived from DNA library genomic, DNA sequence. A2527678 A2527678.1 GI:11079801 Seq primer: M13-Reverse Class: shotgun Entamoeba histolytica. 1. .912

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Seg primer: M13-
Class: shotgun
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EWRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial ECORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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BACR29P01 of RPCI-98 library from Droscophila melanogaster (fruit fly), genomic survey sequence.
                                                                                                                                                        481 AATGTTTATTTAAACATCCAATTCATAGGCTTATAAATATTAATGTGTATATTTTATCAA 540
                                                                                                                                                                                                                                                                                                                                                                                                                        179 AATGAATATTTAACATTGAAAATGTTGATTTTATTTTAATATTTTGTTCAACATAAAATCAA 238
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                                                                                                                                                                                                                                                                                                                 601 ACTCATAAAAACCCACACAATGTGAAGCTCTGTTATAAATGGGTGCCATGTAAGATGGAA
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
                                                                          Score 52; DB 245;
Pred. No. 0.07;
0; Mismatches 155;
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Best Local Similarity 48.3
Matches 145; Conservative
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/db_xref="taxon:5759"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/clone_lib="Define the property of the profession of the professi
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Tel: 301 838 0200
Tel: 31838 0200
Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
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Entamoeba histolyfica:
Eukaryota; Entamoebidae; Entamoeba.

1 (bases 1 to 853)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica HM1:NSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                     621 ТАТААМНТИТАААТТТАТАМТТИАМАТТТТАААТАМАТТТААИТТААМТТАМИТИТТААМ 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 CAATTCTAATTTAATGTATATTAAAAATTCCTCTGCAAATATGTGAGGAGGGACCTCATA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AAATATTGTCATATGGAAATGAGCAGATAATAAAGATTATAGCTTTTCTTTGTCAAAAGG 240
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Length 1101;
6.0%; Score 52; DB 219; Length 1 37.3%; Pred. No. 0.071; Live 44; Mismatches 136; Indels
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High quality sequence stop: 838.
Location/Qualiflers
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Search completed: November 20, 2001, 15:31:57 Job time: 3966 sec
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//Clone_Wector: pHOS1; Site_1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
GG., and Diamond, L.S. (1993) Entanobea histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
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1 (bases 1 to 868)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HMI:IMSS sheared DNA library
  Vaudin and
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Sequencing: A Practical Approach, eds. M. Barell, Oxford University Press, 1999)."
                                                                                                                     Score 51.8; DB 245; Length
Pred. No. 0.077;
0; Mismatches 127; Indels
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Contact: Brendan J Loftus
Department of Enkaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD
Tel: 301 838 0208
Fax: 301 838 0208
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High quality sequence stop: 779.
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Seq primer: M13-Reverse
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50.2%;
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tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barell, Oxford University Press, 1999)."
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                                                                                                                                                                                         DB 248;
                                                                                                                                                                                       Score 51.8; DB 248;
Pred. No. 0.077;
0; Mismatches 127;
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Best Local Similarity
Matches 128; Conserv
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